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ATTENUATED RESPIRATORY SYNCYTIAL VIRUSES*Inv'd*  
Field Of The Invention

5           This invention relates to respiratory  
syncytial viruses of subgroup B having at least one  
attenuating mutation in the RNA polymerase gene. This  
invention was made with Government support under a  
grant awarded by the Public Health Service. The  
10       Government has certain rights in the invention.

Background Of The Invention

15           Respiratory syncytial virus (RSV) is a  
nonsegmented, negative-sense, single stranded enveloped  
RNA virus. RSV belongs to the Family Paramyxoviridae,  
the Subfamily Pneumovirinae and the genus *Pneumovirus*.  
Pneumoviruses have 10 protein-encoding cistrons. These  
proteins in RSV are the nucleocapsid protein N, the  
20       phosphoprotein P, the nonglycosylated virion matrix  
protein M, the attachment protein G, the fusion protein  
F, the polymerase protein L, the nonstructural proteins  
NS1 and NS2, the small hydrophobic protein SH, and the  
transcription elongation factor protein M2.

25           The genomic RNA of RSV serves two template  
functions in the context of a nucleocapsid: as a  
template for the synthesis of messenger RNAs (mRNAs)  
and as a template for the synthesis of the antigenome  
(+) strand. RSV encodes and packages its own RNA  
30       dependent RNA Polymerase. Messenger RNAs are only  
synthesized once the virus has been uncoated in the  
infected cell. Viral replication occurs after  
synthesis of the mRNAs and requires the continuous  
synthesis of viral proteins. The newly synthesized  
35       antigenome (+) strand serves as the template for

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generating further copies of the (-) strand genomic RNA.

The polymerase complex actuates and achieves transcription and replication by engaging the cis-acting signals at the 3' end of the genome, in particular, the promoter region. Viral genes are then transcribed from the genome template unidirectionally from its 3' to its 5' end. There is always less mRNA made from the downstream genes (e.g., the polymerase gene (L)) relative to their upstream neighbors (i.e., the nucleoprotein gene (N)). Therefore, there is always a gradient of mRNA abundance according to the position of the genes relative to the 3'-end of the genome.

RSV is the leading cause of viral pneumonia and bronchiolitis in infants and young children and is responsible for an estimated 95,000 hospitalizations and 4,500 deaths per year in the United States (Bibliography entries 1,2,3). Serious disease is most prevalent in infants 6 weeks to 6 months of age and in children with certain underlying illnesses (e.g. immunodeficiencies, congenital heart disease and bronchopulmonary dysplasia).

Two major subgroups of RSV have been identified, A and B, as well as antigenic variants within each subgroup (4). Multiple variants of each subgroup have been found to cocirculate in epidemics which occur annually during late fall, winter, and spring months (5). Most children are infected by two years of age. Complete immunity to RSV, however, does not develop and reinfections occur throughout life (6,7). These reinfections often are symptomatic, though generally confined to mild upper respiratory tract disease. A decrease in severity of disease is associated with two or more prior infections and, in some studies, with high levels of serum antibody,

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suggesting that protective immunity to RSV disease will accumulate following repeated infections (2,6,8,9,10,11). There is also evidence that children infected with one of the two major RSV subgroups may be somewhat protected against reinfection with the homologous subgroup (12). These observations suggest that it is both possible and worthwhile to develop an RSV vaccination regimen for infants and young children which would provide sufficient temporary immunity to protect against severe disease and death.

The identification of the two major subgroups of RSV has been based on reactivities of the F and G surface glycoproteins with monoclonal antibodies (4,13) and further delineated by sequence analysis (14,15). Both F and G proteins elicit neutralizing antibodies and immunization with these proteins provides protection against reinfection in mouse and cotton rat models (16,17,18). Most neutralizing antibodies are directed against the F protein. Beeler and Coelingh reported that out of 16 neutralization epitopes mapped to the F protein, 8 epitopes were conserved in all or all but one of 23 virus isolates tested (19). A high degree of sequence homology exists between the F protein of subgroups A and B (approximately 90% amino acid and approximately 80% nucleotide) whereas a much lower degree of homology exists between the G proteins (approximately 50-60% amino acid and approximately 60-70% nucleotide) (14). Correspondingly, immunity elicited by the F protein is more crossprotective between subgroups than is immunity elicited by the G protein (16,17). In mice, humoral immunity induced by both the F and G proteins is thought to be responsible for protection against reinfection with virus (20) whereas the CTL response is thought to be more important in resolution of primary infections

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(21,22,23). The M2 (or 22K) protein has been shown to be a potent inducer of cytotoxic lymphocytes (CTL) in mice, with lesser CTL recognition of F, N, and P proteins (24,25). Human CTL's have been shown to recognize the F, M2, N, M, SH, and NS2 (or 1b) proteins (26). These data suggest that the F protein of either virus subgroup is a crucial immunogen in any RSV vaccine and that the G, M2, N, M, SH, and NS2 proteins should also be considered potential vaccine components.

For RSV, no vaccines of any kind are currently available. Thus, there is a need to develop vaccines against this human pathogen. Such vaccines would have to elicit an immune response in the recipient which will prevent serious RSV disease, i.e., LRD. The qualitative and quantitative features of such a favorable response are extrapolated from those seen in survivors of natural virus infection, who, though not protected from reinfection by the same or highly related viruses, are protected from serious or fatal disease.

A variety of approaches can be considered in seeking to develop such vaccines, including the use of: (1) purified individual viral protein vaccines (subunit vaccines); (2) inactivated whole virus preparations; and (3) live, attenuated viruses.

Subunit vaccines have the desirable feature of being pure, definable and relatively easily produced in abundance by various means, including recombinant DNA expression methods. To date, with the notable exception of hepatitis B surface antigen, viral subunit vaccines have generally only elicited short-lived and/or inadequate immunity, particularly in naive recipients.

Formalin inactivated whole virus preparations of polio (IPV) and hepatitis A have proven safe and

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efficacious. In contrast, immunization with similarly inactivated whole RSV elicited unfavorable immune responses and/or response profiles which predisposed vaccinees to exaggerated or aberrant disease when subsequently confronted with the natural or "wild-type" virus.

Early attempts (1966) to vaccinate young children used a parenterally administered formalin-inactivated RSV vaccine. Unfortunately, several field trials of this vaccine revealed serious adverse reactions - the development of a severe illness with unusual features following subsequent natural infection with RSV (27,28). It has been suggested that this exposure to formalinized RSV antigen elicited an abnormal or unbalanced immune response profile, predisposing the vaccinee to RSV disease potentiation (29,30).

Several different live, attenuated viruses have proven remarkably effective as a means of achieving immunoprophylaxis. Pursuit of such vaccine candidates for RSV has been intense and long-standing.

RSV temperature sensitive (*ts*) mutants derived by chemical mutagenesis (31) were shown to be attenuated in rodent and non-human primate models (32,33).

Cold adaptation, a process by which virus is adapted to growth at temperatures colder than those at which it normally optimally grows, has been used to develop attenuated *ts* virus mutants for use as vaccines (for review see (34)). This method generally results in the accumulation of multiple genetic lesions which may help to confer phenotypic stability by reducing the probability that reversion of any one lesion will result in reversion of the relevant phenotype. Maassab has used stepwise cold adaptation to successfully

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develop several ts influenza vaccine candidates currently in clinical trials (35,36,37). These mutants, which bear attenuating mutations in at least four different genes, appear to be attenuated, immunogenic, and phenotypically stable.

Belshe and co-workers have used cold adaptation to develop attenuated, ts strains of a paramyxovirus, parainfluenza virus type 3 (38,39). In this case, cold adaptation was carried out in primary African green monkey kidney cells by reducing temperatures to 20°C. Analysis of several virus variants cloned from this cold adapted population demonstrated that the level of attenuation and temperature sensitivity increased as the length of cold adaptation increased. These variants were shown to have reduced potential for virulence in humans, however the temperature sensitive phenotype was somewhat unstable in clinical trials (40).

RSV was successfully cold adapted to 25-26°C in several laboratories in the mid 1960's, but was found to be under-attenuated in vaccine trials (34,41,42). Maassab and DeBorde (34) have suggested this may be because cold adaptation was not carried out at low enough temperatures, or clones of adequately attenuated virus were not isolated from a genetically mixed population of cold-adapted virus.

Nevertheless, this means for generating attenuated live RSV vaccine candidates is lengthy and, at best, unpredictable, relying largely on the selective outgrowth of those randomly occurring genomic mutants with desirable attenuation characteristics. The resulting viruses may have the desired phenotype in vitro, and even appear to be attenuated in animal models. However, all too often they remain either under- or overattenuated in the human or animal host

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for whom they are intended as vaccine candidates.

Thereafter, two live, attenuated RSV mutants were generated by cold passage or chemical mutagenesis.

These RSV strains were found to have reduced virulence in seropositive adults. Unfortunately, they proved either over- or underattenuated when given to seronegative infants; in some cases they were also found to lack genetic stability (43,44). Another vaccination approach using parenteral administration of live virus was found ineffective and efforts along this line were discontinued (45). Notably, these live RSV vaccines were never associated with disease enhancement as observed with the formalin-inactivated RSV vaccine described above.

Currently, there are no RSV vaccines approved for administration to humans, although clinical trials are now in progress with cold-passaged, chemically mutagenized strains of RSV designated A2 and B-1.

Appropriately attenuated live derivatives of wild-type viruses offer a distinct advantage as vaccine candidates. As live, replicating agents, they initiate infection in recipients during which viral gene products are expressed, processed and presented in the context of the vaccinee's specific MHC class I and II molecules, eliciting humoral and cell-mediated immune responses, as well as the coordinate cytokine patterns, which parallel the protective immune profile of survivors of natural infection.

This favorable immune response pattern is contrasted with the delimited responses elicited by inactivated or subunit vaccines, which typically are largely restricted to the humoral immune surveillance arm. Further, the immune response profile elicited by some formalin inactivated whole virus vaccines, e.g., measles and respiratory syncytial virus vaccines

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developed in the 1960's, have not only failed to provide sustained protection, but in fact have led to a predisposition to aberrant, exaggerated, and even fatal illness, when the vaccine recipient later confronted the wild-type virus.

While live, attenuated viruses have highly desirable characteristics as vaccine candidates, they have proven to be difficult to develop. The crux of the difficulty lies in the need to isolate a derivative of the wild-type virus which has lost its disease-producing potential (i.e., virulence), while retaining sufficient replication competence to infect the recipient and elicit the desired immune response profile in adequate abundance.

Historically, this delicate balance between virulence and attenuation has been achieved by serial passage of a wild-type viral isolate through different host tissues or cells under varying growth conditions (such as temperature). This process presumably favors the growth of viral variants (mutants), some of which have the favorable characteristic of attenuation. Occasionally, further attenuation is achieved through chemical mutagenesis as well.

This propagation/passage scheme typically leads to the emergence of virus derivatives which are temperature sensitive, cold-adapted and/or altered in their host range -- one or all of which are changes from the wild-type, disease-causing viruses -- i.e., changes that are associated with attenuation.

Rational vaccine design would be assisted by a better understanding of RSV, in particular, by the identification of the virally encoded determinants of virulence as well as those genomic changes which are responsible for attenuation.



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Summary Of The Invention

Accordingly, it is an object of this invention to identify those regions of the polymerase gene of RSV subgroup B where mutations result in attenuation of those viruses.

It is a further object of this invention to produce recombinantly-generated RSV subgroup B which incorporate such attenuating mutations in their genomes.

It is still a further object of this invention to formulate vaccines containing such attenuated viruses.

These and other objects of the invention as discussed below are achieved by the generation and isolation of recombinantly-generated, attenuated, RSV subgroup B having at least one attenuating mutation in the RNA polymerase gene.

The at least one attenuating mutation in the RNA polymerase gene is selected from the group consisting of nucleotide changes which produce changes in an amino acid selected from the group consisting of residues 353 (arginine → lysine), 451 (lysine → arginine), 1229 (aspartic acid → asparagine), 2029 (threonine → isoleucine) and 2050 (asparagine → aspartic acid).

In another embodiment of this invention, attenuated virus is used to prepare vaccines which elicit a protective immune response against the wild-type form of the virus.

In yet another embodiment of this invention, an isolated, positive strand, antigenomic message sense nucleic acid molecule (or an isolated, negative strand genomic sense nucleic acid molecule) having the

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complete viral nucleotide sequence (whether of wild-type virus or virus attenuated by non-recombinant means) is manipulated by introducing one or more of the attenuating mutations described in this application to generate an isolated, recombinantly-generated attenuated virus. This virus is then used to prepare vaccines which elicit a protective immune response against the wild-type form of the virus.

In still another embodiment of this invention, such a complete wild-type or vaccine viral nucleotide sequence (as well as a revertant sequence) is used: (1) to design PCR primers for use in a PCR assay to detect the presence of the corresponding virus in a sample; or (2) to design and select peptides for use in an ELISA to detect the presence of the corresponding virus in a sample.

#### Brief Description Of The Figures

Figure 1 shows a flow chart detailing the propagation of RSV 2B working seed MK7V14b and RSV 3A working seed MK8V17b.

Figure 2 shows growth and cytopathic effect of RSV 2B at temperatures from 26°C to 36°C in Vero cells.

Figure 3 shows growth and cytopathic effect of RSV 3A at temperatures from 26°C to 36°C in Vero cells.

Figure 4 graphically shows titration results obtained at each passage of RSV 2B and RSV 3A.

Figure 5 shows the growth curves of RSV 2B, RSV 2Bp24G, RSV 2Bp20L, RSV 3A, RSV 3Ap20E and RSV 3Ap20F in Vero cells at temperatures from 20°C to 40°C.

Figure 6 compares graphically the growth of

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RSV 2B and RSV 2Bp20L in cotton rats from 3 to 7 days post-infection.

Figure 7 compares the relative growth and pathogenicity of RSV 2B and RSV 2Bp20L in four (4) year old seropositive chimps.

Figure 8 is a diagram showing virus titrations for monkeys infected with the RSV 2B ts mutants and subsequently challenged with the parental strain.

Figure 9 is a diagram showing virus growth in African green monkey cells infected with the RSV 3A ts mutants and challenged with the parental 3A strain.

Figure 10 is a diagram showing a growth study in African green monkeys comparing TS-1 with RSV 2Bp33F and 3Ap28F.

Figure 11 depicts a genetic map of the RSV subgroup B wild-type strains designated 2B and 18537 (top portion), the intergenic sequences of those strains (middle portion) and the 68 nucleotide overlap between the M2 and L genes (bottom portion). The RSV 2B strain has six fewer nucleotides in the G gene, encoding two fewer amino acid residues in the G protein, as compared to the 18537 strain. The 2B strain has 145 nucleotides in the 5' trailer region, as compared to 149 nucleotides in the 18537 strain. The 2B strain has one more nucleotide in each of the NS-1, NS-2 and N genes, and one fewer nucleotide in each of the M and F genes, as compared to the 18537 strain.

#### Detailed Description Of The Invention

The first step in the identification of attenuating mutations in the L gene of RSV subgroup B vaccine strains was the generation of those strains from wild-type strains. The original RSV subgroup B

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vaccine strains (as well as subgroup A vaccine strains) were generated by cold adaptation of the wild-type virus. Cold adaptation comprises obtaining live virulent virus derived from clinical isolates that have been isolated in primary rhesus monkey kidney cells. These are then passed in Vero cells at 35-36°C and plaque purified. Preferably, the Vero cells are passage 133 to 148 of the Vero cell line CCL81, obtained from the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland, U.S.A. 20852. The maintenance medium is preferably MEM with 2% FBS, L-glutamine, non-essential amino acids and 20mM Hepes pH 7.5, and the freezing medium is MEM with 10% FBS and 20mM Hepes pH 7.5.

A confluent monolayer of Vero cells is inoculated with about 1.0 ml of virus inoculum, and virus is allowed to absorb for about one to two hours (preferably, 70 to 120 minutes, and most preferably 90 minutes) at ambient temperature (about 18°C to about 25°C).

The virus flask is incubated at about 18°C to about 26°C, preferably about 20°C, for about two to fifteen days. Virus is harvested by removing the medium and replacing it with freezing medium. The flask is then frozen directly at -70°C, then thawed in a 32°C water bath.

A portion (about 1 ml) is removed from the freeze-thaw lysate and is used to inoculate Vero cells; the process is then repeated. The remaining freeze-thaw lysate is stored at -70°C. It can be used to perform virus titrations and plaque purify virus.

To plaque purify virus, the freeze-thaw lysate is thawed in a 32°C water bath. About three to five serial dilutions of the lysate are made in the maintenance medium. Six-well, twenty-four well, or

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ninety-six well plates containing confluent Vero cells are rinsed with a phosphate buffered saline solution. Wells are inoculated with virus dilution, using only enough volume to cover the bottom of the well. Virus inoculum is adsorbed for 90 minutes at ambient temperature. Wells are overlaid with 1% methylcellulose in MEM-maintenance medium. Plates are incubated at 32°C for five days. Isolated plaques are identified microscopically by looking for typical syncytial plaques, and wells are marked. Plaques are picked at marked sites using small bore pipette or pipette tip and are emulsified in 0.5 ml maintenance medium for 1-3 hours at 4°C. Picked plaques are used to inoculate duplicates of 25 cm<sup>2</sup> flask or 96-well plates containing Vero cell monolayers as described above. Duplicate inoculated flasks or plates are overlaid with maintenance medium. One duplicate is incubated at 32°C and the other at 39°C for 5-10 days. Flasks or plates incubated at 32°C are examined microscopically for virus cytopathic effect (CPE). Flasks or plates incubated at 39°C are stained by immunoperoxidase assay for RSV specific antigen. Flasks or plates which demonstrate easily detectable CPE at 32°C and little or no detectable RSV antigen by immunoperoxidase staining are selected as containing temperature sensitive (ts) mutants. Virus from the selected flask or plate described above are harvested by freeze-thaw technique. This virus represents a plaque purified mutant.

Cold adaptation as just described was used to develop attenuated strains of RSV from two parental strains derived from clinical isolates. Seven ts mutants were isolated, four from a subgroup B virus (RSV 2B) and three from a subgroup A virus (RSV 3A). All seven mutants displayed a temperature sensitive

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phenotype in Vero cell culture, each with unique characteristics. All mutants were attenuated in growth in cotton rats, but displayed different phenotypes. Growth of one of the *ts* mutants, RSV 2Bp20L, was shown to be attenuated in seropositive chimpanzees. All seven mutants retained two major neutralization epitopes.

Cold adaptation of RSV had previously been done in primary or diploid cell lines (bovine embryonic kidney, WI38, and cercopithecus monkey kidney) at temperatures beginning at 34°C-37°C and decreasing to 25°C-26°C. No attempt had been made to isolate multiple individual mutant phenotypes from the cold-adapted virus (37,46,47).

The approach described herein to cold-adapting RSV differed in several significant ways from these previous attempts. This procedure started with a subgroup A and subgroup B virus of different strains than those used previously. These strains bore distinct phenotypic differences from the reference strains and each other. These strains were passed several times to adapt virus to Vero cells and to plaque purify virus. Virus was passaged in a continuous cell line, Vero cells, rather than a diploid or primary cell line. Several strategies of temperature change were used, to provide a greater potential for isolation of a variety of mutant phenotypes.

Unlike previous RSV cold adaptation strategies where cold adaptation had started at 34-37°C and gone down to 25-26°C, cold adaptation started at either 26°C (since it was found that the parental strains grew well at this temperature) or 22°C, and gradually reduced the growth temperature to 20°C. Passage strategies attempted to cover both the

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recommendation of "slow" adaptation to very low temperatures as proposed by Massab and DeBorde (37), as well as efforts to try a faster and more aggressive approach. RNA viruses mutate at such a high frequency that any population of virus will contain a number of individual virus variants (48). Therefore, a variety of virus mutants were isolated from individual flasks at various virus passage levels and from different cold adaptation strategies.

The results were interesting and somewhat unexpected. The rate at which virus became adapted (i.e., grew to consistently high titers at the 20°C temperature), was most affected by the strain of virus used, implying a significant host-related factor in adaptation. RSV 2B easily adapted to the cold temperatures, even using a rapid adaptation scheme. In contrast, RSV 3A grew poorly at the low temperatures. RSV 3A was eventually cold-adapted using the slow passage scheme, but the more rapid adaptation approaches did not appear promising and were discontinued. Based on cold adaptation experiences reported by other researchers, it was expected *ts* mutants would arise and eventually become the predominant virus variants in the cold-adapted populations. For example, Belshe and Hissom (41) reported that with parainfluenza virus type 3 adapted to grow at 20°C, 80% of plaque purified virus clones were *ts* by passage 18 and 100% were *ts* by passage 45. In this study, even after 38-40 low temperature passages, including up to 32 passages done at 20°C, RSV *ts* mutants remained a minor population. This would suggest that *ts* and cold-adapted phenotypes may not be as strongly linked in RSV as they are in other viruses.

The level of attenuation is a critical factor in developing vaccines for any target population and is

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of particular importance for vaccines intended for infants and young children. Virus must be sufficiently attenuated to not cause disease, yet grow well enough in the vaccine to elicit protective immunity.

5           Widely accepted markers for attenuation are *ts* phenotype and reduced growth in animal models. However, these markers are only approximate and testing must eventually be done in the target population. The RSV 3A *ts* mutants could be distinguished from the RSV 10 3A parental virus by reduced replication in both the nose and lungs. Also of note, although the RSV 3A parental virus grew much better in the nose than the lungs of cotton rats, virus recovery was similar in both nose and lungs of BALB/c mice. These data suggest 15 that the attenuation seen in cotton rats is due to more than one factor, and that this factor is not directly related to temperature sensitivity as measured in vitro. The cotton rat is relatively nonpermissive for growth of RSV and disease does not develop, suggesting 20 that this model is an unreliable indicator of level of attenuation in humans.

          In contrast, chimpanzees are highly susceptible to RSV infection and develop an upper and lower respiratory tract disease that is very similar to 25 that seen in humans. In seropositive chimps, it was found that the RSV 2B parental strain caused mild upper respiratory tract disease similar to that caused by natural RSV infections in adult humans. The RSV 2Bp20L mutant did not grow, clearly demonstrating that this *ts* 30 mutant was attenuated in a permissive host as well as the non-permissive cotton rat. The level of attenuation is best assessed in a seronegative chimp, as prior virus exposure will affect the host response to virus challeng . Unfortunately, testing in 35 seronegative chimps is severely hampered by the limited

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availability of these animals.

The mutants described herein bear the desirable traits of an attenuated, phenotypically stable, and immunogenic RSV vaccine virus in the human target population.

The immunopotency of the recombinantly-generated RSV subgroup B vaccine is determined by monitoring the immune response of test animals following immunization with the vaccine. Test animals include, but are not limited to, mice, rats (e.g., cotton rats), rabbits, primates, e.g., African green monkeys, chimps, and human subjects. Methods of introduction of the immunogen may include oral, parenteral, topical, intranasal or any other standard routes of immunizations. The immune response of the test subjects is analyzed by four approaches: (a) the reactivity of the resultant immune serum to authentic RSV antigens, as assayed by known techniques, e.g., enzyme linked immunosorbant assay (ELISA), immunoblots, radioimmunoprecipitations, etc.; (b) the ability of the immune serum to neutralize RSV infectivity *in vitro*; (c) the ability of the immune serum to inhibit virus fusion *in vitro*; and (d) protection from RSV infection or significant disease.

The cold-adapted RSV mutants are capable of eliciting an immune response when administered to a subject without causing significant disease, such as respiratory distress or otitis media. As used herein, the term "cold-adapted mutant" means an attenuated virus that has been attenuated by propagation at lower than optimal temperatures. Examples of cold-adapted mutant viruses have been provided as described above. The cold-adapted mutant RSV may be a mutant of subgroup A, such as the group consisting of 3Ap20E, 3Ap20F and 3Ap28F. The cold-adapted mutant RSV may also be a

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mutant of the subgroup B, such as the group consisting of 2Bp33F, 2Bp24G, 2Bp20L and 2Bp34L. The subgroup B viruses are then sequenced and differences between wild-type and mutant strains are identified. Those mutations which contribute to the attenuated phenotype are then assessed.

Transcription and replication of negative-sense, single stranded RNA viral genomes such as RSV subgroup B are achieved through the enzymatic activity of a multimeric protein acting on the ribonucleoprotein core (nucleocapsid). Naked genomic RNA cannot serve as a template. Instead, these genomic sequences are recognized only when they are entirely encapsidated by the N protein into the nucleocapsid structure. It is only in that context that the genomic and antigenomic terminal promoter sequences are recognized to initiate the transcriptional or replication pathways.

All paramyxoviruses require the two viral proteins, L and P, for these polymerase pathways to proceed. The pneumoviruses, including RSV, also require the transcription elongation factor M2 for the transcriptional pathway to proceed efficiently. Additional cofactors may also play a role, including perhaps the virus-encoded NS1 and NS2 proteins, as well as perhaps host-cell encoded proteins.

However, considerable evidence indicates that it is the L protein which performs most if not all the enzymatic processes associated with transcription and replication, including initiation, and termination of ribonucleotide polymerization, capping and polyadenylation of mRNA transcripts, methylation and perhaps specific phosphorylation of P proteins. The L protein's central role in genomic transcription and replication is supported by its large size, sensitivity to mutations, and its catalytic level of abundance in

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the transcriptionally active viral complex (49).

These considerations led to the proposal that L proteins consist of a linear array of domains whose concatenated structure integrates discrete functions (50). Indeed, three such delimited, discrete elements within the negative-sense virus L protein have been identified based on their relatedness to defined functional domains of other well-characterized proteins. These include: (1) a putative RNA template recognition and/or phosphodiester bond formation domain; (2) an RNA binding element; and (3) an ATP binding domain. All prior studies of L proteins of nonsegmented negative-sense, single stranded RNA viruses have revealed these putative functional elements (50).

In summary, the invention comprises the identification of changes in the polymerase gene (L) which result in attenuation of the virus while retaining sufficient ability of the virus to replicate. Attenuation is optimized by rational mutations of the polymerase gene, which provide the desired balance of replication efficiency: so that the virus vaccine is no longer able to produce disease, yet retains its capacity to infect the vaccinee's cells, to express sufficiently abundant gene products to elicit the full spectrum and profile of desirable immune responses, and to reproduce and disseminate sufficiently to maximize the abundance of the immune response elicited.

Animal studies have demonstrated a decrease in viral replication sufficient to avoid illness but adequate to elicit the desired immune response. This likely represents a decrease in transcription, a decrease in gene expression of virally encoded proteins, a decrease in antisense templates and, therefore, the production of fewer new genomes. The

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resulting attenuated viruses are significantly less virulent than the wild-type.

The attenuating mutations described herein may be introduced into viral strains by two methods:

5 (1) Conventional means such as chemical mutagenesis during virus growth in cell cultures to which a chemical mutagen has been added, selection of virus that has been subjected to passage at suboptimal temperature in order to select temperature sensitive and/or cold-adapted mutations, identification of mutant virus that produce small plaques in cell culture, and passage through heterologous hosts to select for host range mutations. These viruses are then screened for attenuation of their biological activity in an animal model. Attenuated viruses are subjected to nucleotide sequencing of their polymerase genes to locate the sites of attenuating mutations. Once this has been done, method (2) is then carried out.

10 (2) A preferred means of introducing attenuating mutations comprises making predetermined mutations using site-directed mutagenesis. These mutations are identified either by method (1) or by reference to closely-related viruses whose attenuating mutations are already known. One or more mutations are introduced into the polymerase gene. Cumulative effects of different combinations of coding and non-coding changes can also be assessed.

20 The mutations to the polymerase gene are introduced by standard recombinant DNA methods into a DNA copy of the viral genome. This may be a wild-type or a modified viral genome background (such as viruses modified by method (1)), thereby generating a new virus. Infectious clones or particles containing these attenuating mutations are generated using the cDNA "rescue" system, which has been applied to a variety of

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viruses, including Sendai virus (51); measles virus (52); respiratory syncytial virus (53); rabies (54); vesicular stomatitis virus (VSV) (55); and rinderpest virus (56); these references are hereby incorporated by reference. See, for RSV rescue, published International patent application WO 97/12032, designating the United States (57); this application is hereby incorporated by reference.

Briefly, all Mononegavirales rescue systems can be summarized as follows: Each requires a cloned DNA equivalent of the entire viral genome placed between a suitable DNA-dependent RNA polymerase promoter (e.g., the T7 RNA polymerase promoter) and a self-cleaving ribozyme sequence (e.g., the hepatitis delta ribozyme) which is inserted into a propagatable bacterial plasmid. This transcription vector provides the readily manipulable DNA template from which the RNA polymerase (e.g., T7 RNA polymerase) can faithfully transcribe a single-stranded RNA copy of the viral antigenome (or genome) with the precise, or nearly precise, 5' and 3' termini. The orientation of the viral genomic DNA copy and the flanking promoter and ribozyme sequences determine whether antigenome or genome RNA equivalents are transcribed. Also required for rescue of new virus progeny are the virus-specific trans-acting proteins needed to encapsidate the naked, single-stranded viral antigenome or genome RNA transcripts into functional nucleocapsid templates: the viral nucleocapsid (N or NP) protein, the polymerase-associated phosphoprotein (P) and the polymerase (L) protein. These proteins comprise the active viral RNA-dependent RNA polymerase which must engage this nucleocapsid template to achieve transcription and replication.

The trans-acting proteins required for RSV

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rescue are the encapsidating protein N, the polymerase complex proteins, P and L, and an additional protein, M2, the RSV-encoded transcription elongation factor.

Typically, these viral trans-acting proteins are generated from one or more plasmid expression vectors encoding the required proteins, although some or all of the required trans-acting proteins may be produced within mammalian cells engineered to contain and express these virus-specific genes and gene products as stable transformants.

The typical (although not necessarily exclusive) circumstances for rescue include an appropriate mammalian cell milieu in which T7 polymerase is present to drive transcription of the antigenomic (or genomic) single-stranded RNA from the viral genomic cDNA-containing transcription vector. Either cotranscriptionally or shortly thereafter, this viral antigenome (or genome) RNA transcript is encapsidated into functional templates by the nucleocapsid protein and engaged by the required polymerase components produced concurrently from co-transfected expression plasmids encoding the required virus-specific trans-acting proteins. These events and processes lead to the prerequisite transcription of viral mRNAs, the replication and amplification of new genomes and, thereby, the production of novel viral progeny, i.e., rescue.

For the rescue of rabies, VSV and Sendai, T7 polymerase is provided by recombinant vaccinia virus VTF7-3. This system, however, requires that the rescued virus be separated from the vaccinia virus by physical or biochemical means or by repeated passaging in cells or tissues that are not a good host for poxvirus. For measles virus (MV) cDNA rescue, this requirement is avoided by creating a cell line that

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expresses T7 polymerase, as well as viral N and P proteins. Rescue is achieved by transfecting the genome expression vector and the L gene expression vector into the helper cell line. Advantages of the host-range mutant of the vaccinia virus, MVA-T7, which expresses the T7 RNA polymerase, but does not replicate in mammalian cells, are exploited to rescue RSV, Rinderpest virus and MV. After simultaneous expression of the necessary encapsidating proteins, synthetic full length antigenomic viral RNA are encapsidated, replicated and transcribed by viral polymerase proteins and replicated genomes are packaged into infectious virions. In addition to such antigenomes, genome analogs have now been successfully rescued for Sendai and PIV-3 (58,59).

The rescue system thus provides a composition which comprises a transcription vector comprising an isolated nucleic acid molecule encoding a genome or antigenome of RSV subgroup B having at least one attenuating mutation in the RNA polymerase gene, together with at least one expression vector which comprises at least one isolated nucleic acid molecule encoding the trans-acting N, P, L and M2 proteins necessary for encapsidation, transcription and replication. Host cells are then transformed or transfected with the at least two vectors just described. The host cells are cultured under conditions which permit the co-expression of these vectors so as to produce the infectious attenuated virus.

The rescued infectious RSV is then tested for its desired phenotype (temperature sensitivity, cold adaptation, plaque morphology, and transcription and replication attenuation), first by *in vitro* means.

If the attenuated phenotype of the rescued

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virus is present, challenge experiments are conducted with an appropriate animal model. Non-human primates provide the preferred animal model for the pathogenesis of human disease. These primates are first immunized with the attenuated, recombinantly-generated virus, then challenged with the wild-type form of the virus. Monkeys are infected by various routes, including but not limited to intranasal or intratracheal routes of inoculation (60). Protection in non-human primates is measured by such criteria as disease signs and symptoms, virus shedding and antibody titers. If the desired criteria are met, the attenuated, recombinantly-generated virus is considered a viable vaccine candidate for testing in humans. The "rescued" virus is considered to be "recombinantly-generated", as are the progeny and later generations of the virus, which also incorporate the attenuating mutations.

Even if a "rescued" virus is underattenuated or overattenuated relative to optimum levels for vaccine use, this is information which is valuable for developing such optimum strains.

Optimally, a codon containing an attenuating point mutation may be stabilized by introducing a second or a second plus a third mutation in the codon without changing the amino acid encoded by the codon bearing only the attenuating point mutation. Infectious virus clones containing the attenuating and stabilizing mutations are also generated using the cDNA "rescue" system described above.

Two major subgroups of human RSV, designated A and B, have been identified based on reactivities of the F and G surface glycoproteins with monoclonal antibodies (4). More recently, the A and B lineages of RSV strains have been confirmed by sequence analysis (14,15). Bovine, ovine, and caprine strains of this

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virus have also been isolated. The host specificity of the virus is most clearly associated with the G attachment protein, which is highly divergent between the human and the bovine/ovine strains (61,62), and may be influenced, at least in part, by receptor binding.

RSV is the primary cause of serious viral pneumonia and bronchiolitis in infants and young children. Serious disease, i.e., lower respiratory tract disease (LRD), is most prevalent in infants less than six months of age. It most commonly occurs in the nonimmune infant's first exposure to RSV. RSV additionally is associated with asthma and hyperreactive airways and it is a significant cause of mortality in "high risk" children with bronchopulmonary dysplasia and congenital heart disease (CHD). It is also one of the common viral respiratory infections predisposing to otitis media in children. In adults, RSV generally presents as uncomplicated upper respiratory illness; however, in the elderly it rivals influenza as a predisposing factor in the development of serious LRD, particularly bacterial bronchitis and pneumonia. Disease is always confined to the respiratory tract, except in the severely immunocompromised, where dissemination to other organs can occur. Virus is spread to others by fomites contaminated with virus-containing respiratory secretions, and infection initiates through the nasal, oral, or conjunctival mucosa.

RSV disease is seasonal and virus is usually isolated only in the winter months, e.g., from November to April in northern latitudes. The virus is ubiquitous, and over 90% of children have been infected at least once by 2 years of age. Multiple strains cocirculate. There is no direct evidence of antigenic drift (such as that seen with influenza A viruses), but

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sequence studies demonstrating accumulation of amino acid changes in the hypervariable regions of the G protein and SH proteins suggest that immune pressure may drive virus evolution.

5 In mouse and cotton rat models, both the F and G proteins of RSV elicit neutralizing antibodies and immunization with these proteins alone provides longterm protection against reinfection (16,17).

10 In humans, complete immunity to RSV does not develop and reinfections occur throughout life (6,7); however, there is evidence that immune factors will protect against severe disease. A decrease in severity of disease is associated with two or more prior infections and there is evidence that children infected with one of the two major RSV subgroups may be somewhat protected against reinfection with the homologous subgroup (13), observations which suggest that a live attenuated virus vaccine may provide protection sufficient to prevent serious morbidity and mortality. 15 Infection with RSV elicits both antibody and cell mediated immunity. Serum neutralizing antibody to the F and G proteins has been associated, in some studies, with protection from LRD, although reduction in upper respiratory disease (URD) has not been demonstrated. 20 High levels of serum antibody in infants is associated with protection against LRD, and administration of intravenous immunoglobulin with high RSV neutralizing antibody titers has been shown to protect against severe disease in high risk children (7,10,63). The role of local immunity, and nasal antibody in particular, is being investigated. 25 30

The RSV virion consists of a ribonucleoprotein core contained within a lipoprotein envelope. The virions of pneumoviruses are similar in size and shape to those of all other paramyxoviruses. 35

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When visualized by negative staining and electron microscopy, virions are irregular in shape and range in diameter from 150-300 nm (64). The nucleocapsid of this virus is a symmetrical helix similar to that of other paramyxoviruses, except that the helical diameter is 12-15 nm rather than 18nm. The envelope consists of a lipid bilayer that is derived from the host membrane and contains virally coded transmembrane surface glycoproteins. The viral glycoproteins mediate attachment and penetration and are organized separately into virion spikes. All members of paramyxovirus subfamily have hemagglutinating activity, but this function is not a defining feature for pneumoviruses, being absent in RSV but present in PVM (65). Neuraminidase activity is present in members of the genera Paramyxovirus, Rubulavirus, and is absent in Morbillivirus and Pneumovirus of mice (PVM) (65).

RSV possesses two subgroups, designated A and B. The wild-type RSV (strain 2B) genome is a single strand of negative-sense RNA of 15,218 nucleotides (SEQ ID NO:1) that are transcribed into ten major subgenomic mRNAs. Each of the ten mRNAs encodes a major polypeptide chain: Three are transmembrane surface proteins (G, F and SH); three are the proteins associated with genomic RNA to form the viral nucleocapsid (N, P and L); two are nonstructural proteins (NS1 and NS2) which accumulate in the infected cells but are also present in the virion in trace amounts and may play a role in regulating transcription and replication; one is the nonglycosylated virion matrix protein (M); and the last is M2, another nonglycosylated protein recently shown to be an RSV-specified transcription elongation factor (see Figure 11). These ten viral proteins account for nearly all of the viral coding capacity.

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The viral genome is encapsidated with the major nucleocapsid protein (N), and is associated with the phosphoprotein (P), and the large (L) polymerase protein. These three proteins have been shown to be necessary and sufficient for directing RNA replication of cDNA encoded RSV minigenomes (66). Further studies have shown that for transcription to proceed with full processing, the M2 protein (ORF 1) is required (64). When the M2 protein is missing, truncated transcripts predominate, and rescue of the full length genome does not occur (64).

Both the M (matrix protein) and the M2 proteins are internal virion-associated proteins that are not present in the nucleocapsid structure. By analogy with other nonsegmented negative-stranded RNA viruses, the M protein is thought to render the nucleocapsid transcriptionally inactive before packaging and to mediate its association with the viral envelope. The NS1 and NS2 proteins have only been detected in very small amounts in purified virions, and at this time are considered non-structural. Their functions are uncertain, though they may be regulators of transcription and replication. Three transmembrane surface glycoproteins are present in virions: G, F, and SH. G and F (fusion) are envelope glycoproteins that are known to mediate attachment and penetration of the virus into the host cell. In addition, these glycoproteins represent major independent immunogens (3). The function of the SH protein is unknown, although a recent report has implicated its involvement in the fusion function of the virus (67).

The genomes of two wild-type RSV subgroup B strains (2B and 18537) have now been sequenced in their entirety (see SEQ ID NOS:1 and 3, discussed below). Genomic RNA is neither capped nor polyadenylated (68).

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In both the virion and intracellularly, genomic RNA is tightly associated with the N protein.

The 3' end of the genomic RNA consists of a 44-nucleotide extragenic leader region that is presumed to contain the major viral promoter (68; Fig. 11). The 3' genomic promoter region is followed by ten viral genes in the order 3'-NS1-NS2-N-P-M-SH-G-F-M2-L-5' (Fig. 11). The L gene is followed by a 145-149 nucleotide extragenic trailer region (see Figure 11). Each gene begins with a conserved nine-nucleotide gene start signal 3'-GGGGCAAAAU (except for the ten-nucleotide gene start signal of the L gene, which is 3'-GGGACAAAAAU; differences underlined). For each gene, transcription begins at the first nucleotide of the signal. Each gene terminates with a semi-conserved 12-14 nucleotide gene end (3'-A G U/G U/A ANNN U/A A<sub>3-5</sub>) (where N can be any of the four bases) that directs transcription termination and polyadenylation (Fig. 11). The first nine genes are non-overlapping and are separated by intergenic regions that range in size from 3 to 56 nucleotides for RSV B strains (Fig. 11). The intergenic regions do not contain any conserved motifs or any obvious features of secondary structure and have been shown to have no influence on the preceding and succeeding gene expression in a minireplicon system (Fig. 11). The last two RSV genes overlap by 68 nucleotides (Fig. 11). The gene-start signal of the L gene is located inside of, rather than after, the M2 gene. This 68 nucleotide overlap sequence encodes the last 68 nucleotides of the M2 mRNA (exclusive of the Poly-A tail), as well as the first 68 nucleotides of the L mRNA.

Ten different species of subgenomic polyadenylated mRNAs and a number of polycistronic polyadenylated read-through transcripts are the

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products of genomic transcription (64).

Transcriptional mapping studies using UV light mediated genomic inactivation showed that RSV genes are transcribed in their 3' to 5' order from a single promoter near the 3' end (69). Thus, RSV synthesis appears to follow the single entry, sequential transcription model proposed for all Mononegavirales (70,71). According to this model, the polymerase (L) contacts genomic RNA in the nucleocapsid form at the 3' genomic promoter region and begins transcription at the first nucleotide. RSV mRNAs are co-linear copies of the genes, with no evidence of mRNA editing or splicing.

Sequence analysis of intracellular RSV mRNAs showed that synthesis of each transcript begins at the first nucleotide of the gene start signal (64). The 5' end of the mRNAs are capped with the structure m7G(5')ppp(5')Gp (where the underlined G is the first template nucleotide of the mRNA) and the mRNAs are polyadenylated at their 3' ends (72). Both of these modifications are thought to be made co-transcriptionally by the viral polymerase. Three regions of the RSV 3' genomic promoter have been found to be important as cis acting elements (73). These regions are the first ten nucleotides (presumably acting as a promoter), nucleotides 21-25, and the gene start signal located at nucleotides 45-53 (73). Unlike other Paramyxovirinae, such as measles, Sendai and PIV-3, the remainder of the leader and non-coding region of NS1 gene of RSV was found to be highly tolerant of insertions, deletions and substitutions (73).

Additionally, by saturation mutagenesis (wherein each base is replaced independently by each of the other three bases and compared for translation and replication efficiencies) within the first 12

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nucleotides of the 3' genomic promoter region, a U-tract located at nucleotides 6-10 was shown to be highly inhibitory to substitutions (73). In contrast, the first five nucleotides were relatively tolerant of a number of substitutions and two of them at position four were up-regulatory mutations, resulting in a four- to 20-fold increase in RSV-CAT RNA replication and transcription. Using a bi-cistronic minireplicon system, gene-start and gene-end motifs were shown to be signals for mRNA synthesis and appear to be self contained and largely independent of the nature of adjoining sequence (74).

The L gene start signal lies 68 nucleotides upstream of the M2 gene-end signal, resulting in gene overlap (Fig. 11) (64). The presence of the M2 gene-end signal within the L gene results in a high frequency of premature termination of L gene transcripts. Full length L mRNA is much less abundant and is made when the polymerase fails to recognize the M2 gene-end motif. This results in much lower transcription of L mRNA. The gene overlap seems incompatible with a model of linear sequential transcription. It is not known whether the polymerase that exits the M2 gene jumps backward to the L gene-start signal or whether there is a second, internal promoter for L gene transcription (64). It is also possible that the L gene is accessible by a small fraction of polymerases that fail to start transcription at the M2 gene-start signal and slide down the M2 gene to the L gene-start signal.

The relative abundance of each RSV mRNA decreases with the distance of its gene from the promoter, presumably due to polymerase fall-off during sequential transcription (69). Gene overlap is a second mechanism that reduces the synthesis of full

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length L mRNA. Also, certain mRNAs have features that might reduce the efficiency of translation. The initiation codon for SH mRNA is in a suboptimal Kozak sequence context, while the G ORF begins at the second methionyl codon in the mRNA.

RSV RNA replication is thought (64) to follow the model proposed from studies with vesicular stomatitis virus and Sendai virus (70,71). This involves a switch from the stop-start mode of mRNA synthesis to an antiterminator read-through mode. This results in synthesis of positive sense replication-intermediate (RI) RNA that is an exact complementary copy of genomic RNA. This serves in turn as the template for the synthesis of progeny genomes. The mechanism involved in the switch to the antiterminator mode is proposed to involve cotranscriptional encapsidation of the nascent RNA by N protein (70,71). RNA replication in RSV like other nonsegmented negative-strand RNA viruses is dependent on ongoing protein synthesis (75). Predicted RI RNA has been detected for the standard virus as well as RSV-CAT minigenome (64,75). RI RNA was 10-20 fold less abundant intracellularly than was the progeny genome both for the standard and the minigenome system. The nucleotide sequences (in positive strand, antigenomic, message sense) of various wild-type, vaccine and revertant RSV strains, as well as the deduced amino acid sequences of the RNA polymerase (L protein) of these RSV viruses, are set forth as follows with reference to the appropriate SEQ ID NOS. contained herein:



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<u>Virus</u>	<u>Nucleotide Sequence</u>	<u>L Protein Sequence</u>
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Wild-Type

2B	SEQ ID NO:1	SEQ ID NO:2
18537	SEQ ID NO:3	SEQ ID NO:4

Vaccine

2B33F	SEQ ID NO:5	SEQ ID NO:6
2B20L	SEQ ID NO:7	SEQ ID NO:8

Revertant

2B33F TS(+)	SEQ ID NO:9	SEQ ID NO:10
2B20L TS(+)	SEQ ID NO:11	SEQ ID NO:12

It is noted that the Sequence Listings recite "DNA"; this is necessary for the antigenomic message sense RNA to be provided in full (reciting sequences as "RNA" causes each "T" to be deleted from the sequence).

Each RSV virus genome encodes an L protein that is 2,166 amino acids long. Genome length and other nucleotide information is as follows:

<u>Virus</u>	<u>Genome</u>	<u>L Start Codon</u>	<u>L Stop Codon</u>
<u>Wild-Type</u>	<u>Length</u>		

2B	15218	8502-8504	15000-15002
18537	15229	8509-8511	15007-15009

Vaccine

2B33F	15219	8503-8505	15001-15003
2B20L	15219	8503-8505	15001-15003

Revertant

2B33F TS(+)	15219	8503-8505	15001-15003
2B20L TS(+)	15219	8503-8505	15001-15003

As detailed in Example 8 (especially Tables

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21 and 22) below, the key potentially attenuating sites for the L protein of RSV subgroup B are as follows:

amino acid residues 353 (arginine → lysine), 451

(lysine → arginine), 1229 (aspartic acid →

5 asparagine), 2029 (threonine → isoleucine) and 2050

(asparagine → aspartic acid). It is understood that the nucleotide changes responsible for these amino acid changes are not limited to those set forth in Example 8 below; all changes in nucleotides which result in  
10 codons which are translated into these amino acids are within the scope of this invention.

The attenuated RSV subgroup B viruses of this invention exhibit a substantial reduction of virulence compared to wild-type viruses which infect human and  
15 animal hosts. The extent of attenuation is such that symptoms of infection will not arise in most immunized individuals, but the virus will retain sufficient replication competence to be infectious in and elicit the desired immune response profile in the vaccinee.

20 The attenuated RSV subgroup B viruses of this invention may be used to formulate a vaccine. To do so, the attenuated virus is adjusted to an appropriate concentration and formulated with any suitable vaccine adjuvant, diluent or carrier. Physiologically  
25 acceptable media may be used as carriers. These include, but are not limited to: an appropriate isotonic medium, phosphate buffered saline and the like. Suitable adjuvants include, but are not limited to MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI  
30 ImmunoChem Research, Inc., Hamilton, MT) and IL-12 (Genetics Institute, Cambridge, MA).

In one embodiment of this invention, the formulation including the attenuated virus is intended for use as a vaccine. The attenuated virus may be mixed

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with cryoprotective additives or stabilizers such as proteins (e.g., albumin, gelatin), sugars (e.g., sucrose, lactose, sorbitol), amino acids (e.g., sodium glutamate), saline, or other protective agents. This mixture is maintained in a liquid state, or is then  
5 dessicated or lyophilized for transport and storage and mixed with water immediately prior to administration.

Formulations comprising the attenuated viruses of this invention are useful to immunize a human or animal subject to induce protection against  
10 infection by the wild-type counterpart of the attenuated virus. Thus, this invention further provides a method of immunizing a subject to induce protection against infection by an RSV subgroup B virus  
15 by administering to the subject an effective immunizing amount of a vaccine formulation incorporating an attenuated version of that virus as described hereinabove.

A sufficient amount of the vaccine in an appropriate number of doses must be administered to the  
20 subject to elicit an immune response. Persons skilled in the art will readily be able to determine such amounts and dosages. Administration may be by any conventional effective form, such as intranasally,  
25 parenterally, orally, or topically applied to any mucosal surface such as intranasal, oral, eye, vaginal or rectal surface, such as by an aerosol spray. The preferred means of administration is by intranasal administration.

In another embodiment of this invention, an isolated nucleic acid molecule having the complete viral nucleotide sequence of the wild-type viruses, the vaccine viruses or the revertant viruses described  
30 herein is used to generate oligonucleotide probes (from either positive strand antigenomic message sense or  
35

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negative strand complementary genomic sense) and to express peptides (from positive strand antigenomic message sense only), which are used to detect the presence of those wild-type viruses, vaccine strains and/or revertant strains in samples of body fluids and tissues. The nucleotide sequences are used to design highly specific and sensitive diagnostic tests to detect the presence of the virus in a sample.

Polymerase chain reaction (PCR) primers are synthesized with sequences based on the viral wild-type, vaccine or revertant sequences described herein. The test sample is subjected to reverse transcription of RNA, followed by PCR amplification of selected cDNA regions corresponding to the nucleotide sequence described herein which have nucleotides which are distinct for a defined strain of virus. Amplified PCR products are identified on gels and their specificity confirmed by hybridization with specific nucleotide probes.

ELISA tests are used to detect the presence of antigens of the wild-type, vaccine or revertant viral strains. Peptides are designed and selected to contain one or more distinct residues based on the wild-type, vaccine or revertant sequences described herein. These peptides are then coupled to a hapten (e.g., keyhole limpet hemocyanin (KLH) and used to immunize animals (e.g., rabbits) for the production of monospecific polyclonal antibody. A selection of these polyclonal antibodies, or a combination of polyclonal and monoclonal antibodies can then be used in a "capture ELISA" to detect antigens produced by those viruses.

Samples of mutant RSV described herein have been deposited by Applicants' assignee on March 19, 1992 with the American Type Culture Collection (ATCC)

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12301 Parklawn Drive, Rockville, Maryland, U.S.A.  
20852, under the provisions of the Budapest Treaty for  
the Deposit of Microorganisms for the Purposes of  
Patent Procedures ("Budapest Treaty"). The viruses were  
5 accorded the following ATCC designation numbers:  
2Bp33F(VR 2364), 2Bp24G(VR 2370), 2Bp20L(VR 2368),  
2Bp34L(VR 2365), 3Ap20E(VR 2369), 3Ap20F(VR 2367), and  
3Ap28F(VR 2366). In addition, samples of the 2B wild-  
type RSV virus were deposited by Applicants on August  
10 21, 1997 with the American Type Culture Collection,  
12301 Parklawn Drive, Rockville, Maryland 20852,  
U.S.A., under the provisions of the Budapest Treaty and  
have been assigned ATCC accession number VR2586.

Given these deposited subgroup B strains and  
15 the sequence information for these and other strains  
provided herein, one can use site-directed mutagenesis  
and rescue techniques described above to introduce  
mutations (or restore a wild-type genotype) of all the  
subgroup B strains described herein, as well as taking  
20 these strains and making additional mutations from the  
panel of mutations set forth in Tables 21 and 22 below.

In order that this invention may be better  
understood, the following examples are set forth. The  
examples are for the purpose of illustration only and  
25 are not to be construed as limiting the scope of the  
invention.

### Examples

30 Standard molecular biology techniques are  
utilized according to the protocols described in  
Sambrook et al. (76).

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Example 1Passage and Characterization of RSV 2B  
and RSV 3A Parental Strains

5 RSV 2B and RSV 3A parental strains were isolated and passed in qualified cell lines and under conditions consistent with use as clinical study material.

10 Two RSV strains, 20648 and 23095, were isolated by Dr. Robert Belshe (St. Louis University Health Science Center, St. Louis, MO) from nasal swab samples taken from ill children. These viruses were later recovered from the original frozen nasal swab samples, passed two to three times in primary rhesus monkey kidney (PRMK) cells, and then sent to  
15 applicants.

Isolate 20648 (subgroup B) was renamed RSV 2B. Virus was passed seven times in PRMK cells at 35°C, two times in Vero cells at 35°C and plaque  
20 purified and amplified three times (six passages) in Vero cells at 36°C. Virus was further amplified an additional two times in Vero (36°C), stocks were filtered with a 0.2 m filter and amplified another two times in Vero cells. This was followed by production  
25 of a Master Seed (RSV 2B, MK7 V12b), Intermediate working seed (RSV 2B, MK7 V13b) and Working seed (RSV 2B, MK7 V14b). See Figure 1.

Isolate 23095 (subgroup A) was renamed RSV 3A. RSV 3A was passed eight times in PRMK cells at  
30 35°C. This was followed by two passages in Vero at 35°C and six passages in Vero cells at 36°C, including three plaque purification steps. Virus was further passaged six times in Vero cells at 36°C including a 0.2 m filtration step. This was followed by production  
35 of a Master seed (RSV 3A, MK8 V15b), Intermediate

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working seed (RSV 3A, MK8 V16b), and Working seed (RSV 3A, MK8 V17b). See Figure 1.

Subgroup specificities of RSV 2B and RSV 3A Master seeds were confirmed using subgroup specific monoclonal antibodies. Virus stocks were shown to be free of microbial contaminants and adventitious agents.

The F, N, and G proteins of RSV 2B and RSV 3A stocks and reference RSV strains A2, Long, and 18537 were analyzed by radioimmunoprecipitation (RIP) and western blotting procedures using monoclonal antibodies. The F1 subunits of the RSV subgroup B strains, 2B and 18537, migrated faster on SDS-polyacrylamide gels than did the F1 subunits of the RSV subgroup A strains, 3A and Long. No difference in migration of the N proteins of the RSV 2B and 3A strains and the reference strains was seen. In RIP gels, the G protein was visible as two bands at approximately 80-90 kD and approximately 45 kD. The 80-90 kD bands of RSV 3A and Long comigrated; however, the 80-90 kD band of RSV 2B also appeared to comigrate with the subgroup A species rather than with the faster RSV 18537 (subgroup B1). This suggests that RSV 2B may be a member of the B2 subgroup as described by Akerlind (77). In western blots, the relative proportions of 80-90 kD and 45 kD bands were roughly equal for RSV Long, A2, 2B, and 18537 grown in Vero cells, but staining of the 80-90 kD band of RSV 3A was significantly greater, suggesting a difference in processing of the G protein for this strain when grown in Vero cells. These data demonstrate that the apparent  $M_r$  for the RSV 2B and RSV 3A strains are consistent with current subgroup classifications of RSV, but confirm that these strains are not identical to the prototype RSV reference strains.

Growth of RSV 2B, RSV 3A and RSV A2 in mice

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and in cotton rats was compared. Both RSV 2B and RSV 3A replicated poorly in Balb/c mice compared to the RSV A2 reference strain. Consistent recovery of RSV 2B and RSV 3A could only be obtained at the highest inoculum dose used ( $10^{6.0-6.2}$  PFU), and was similar in magnitude to recovery of RSV A2 at a 100-fold lower inoculum ( $10^{4.3}$  PFU). In contrast, growth of RSV 2B in cotton rat nose and lungs was similar to growth of RSV A2. Growth of RSV 3A in the nose was similar to the other strains; however growth in lungs was significantly poorer. Both mouse and cotton rat growth data indicate that RSV 2B and RSV 3A have significantly different *in vivo* growth characteristics than the RSV A2 reference strain, as well as differing from each other.

#### Example 2

##### Cold Adaptation of RSV

In order to select an appropriate starting temperature for cold adaptation of RSV, growth of the RSV 2B and RSV 3A parental strains in Vero cells at temperatures ranging from 26°C to 36°C was compared. Cells were infected at an MOI of 0.4 and virus yield and CPE was monitored for four days. The results, shown in Figures 2 and 3, demonstrated that for both virus strains, growth at 30°C, 32°C, and 36°C was similar in kinetics and yield. At 26°C, virus growth lagged behind growth at the higher temperatures by about 24 hours. The limiting factor in achieving optimum titers appeared to be the viral CPE, which occurred earlier at higher temperatures. For both RSV 2B and RSV 3A, optimum titers were achieved by maintaining cultures at 30°C. At this temperature, a lower level of CPE allowed growth and spread of virus to continue over a longer time period. The results



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suggested that these strains of RSV were already well adapted to growth at 30°C to 36°C. A maximum temperature of 26°C was selected as a starting temperature for cold adaptation, as virus growth at this temperature was suboptimal and therefore some selective pressure for cold adaptation would be exerted.

Cold adaptation was initiated on virus stocks RSV 2B (passage MK7 V14) and RSV 3A (passage MK8 V14). To maximize the chance of recovering appropriately attenuated mutants from these cold-adapted populations, two flasks of virus were independently passed using each of three different cold adaptation strategies. This provided a total of six cold-adapted populations for RSV 2B and six for RSV 3A. Virus was passaged in 25 cm<sup>2</sup> flasks containing confluent Vero cell monolayers. At each passage, virus was harvested by replacing the maintenance medium (10 mls of MEM/2%FBS/20mMHepes) in the infected flask with a reduced volume of freezing medium (3 mls of MEM/10%FBS/20mMHepes) and performing a quick freeze at -70°C followed by a thaw at 32°C. To infect the next passage, one ml of the freeze-thaw lysate was transferred to a fresh flask of confluent Vero cells, virus was allowed to adsorb at room temperature (20°C-22°C), and then flasks were overlaid with maintenance medium (MEM/2%FBS/20mMHepes) and incubated at the appropriate temperature in water baths (i.e., 26°C, 22°C, 20°C).

Titration were performed at 32°C on each freeze-thaw lysate and the remainder of the material was stored at -70°C for future isolation of virus variants. Three passaging strategies were used. Flasks E and F were "slowly" adapted, beginning at 26°C with four passages every two days, followed by passage once every week until titers appeared to be relatively

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stable or were increasing. Virus was then passaged weekly at 22°C until consistently high titers were achieved, and finally maintained by passage every 1-2 weeks at 20°C. Flasks G, H, and I were adapted by a more moderate strategy. Virus was passaged two times at 26°C at three day intervals, then passaged weekly at 22°C five times, and finally maintained by passage every 1-2 weeks at 20°C. Flasks J and L were "rapidly" adapted, starting with five weekly passages at 22°C, followed by passage at 1-2 week intervals at 20°C. Actual passage conditions and titration results are shown in Tables 1 and 2, and are summarized in Table 3. Titration results obtained at each passage are graphically displayed in Figure 4. The titration results demonstrated an influence of strain on rate of adaptation. For RSV 2B, all three cold adaptation strategies eventually yielded high virus titers when flasks were maintained at 20°C. In contrast, RSV 3A was adapted to growth at 20°C using a "slow" strategy (E,F), but efforts to force a more rapid adaptation resulted in a precipitous decline in virus growth. Passage of these cultures (3A:H,I,J,L) was discontinued.

To screen the cold-adapted virus populations for accumulation of *ts* variants, virus taken from each flask following 5 and 17 weeks of cold adaptation was tested for efficiency of plaquing (EOP) at 39°C vs. 32°C. As seen in Table 4, in most cases plaquing efficiency of the cold passage virus was relatively high at 39°C ( $\geq 0.2$ ) and was similar to values obtained with the parental virus control ( $\geq 0.6$ ). The results showed that the cold-adapted virus populations, with the possible exception of flask RSV 3A-F, had not become predominantly *ts* over a period of up to 17 low temperature passages.

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Following further cold passaging, attempts were made to isolate temperature sensitive mutants by plaque purifying virus from each cold-adapted flask. Plaque purified mutants were initially identified by relatively poor growth (lower titers or smaller plaque size) at 39°C vs 32°C. In these assays, shown in Table 5, the percentage of plaque purified virus that could be clearly identified as temperature sensitive ranged from 0% to 40% of plaques picked. Several individual flasks (2B-H, 2B-L, 3A-E, 3A-F) appeared to contain a relatively higher percent of *ts* phenotypes, and in some cases the percentage of *ts* mutants increased over time. However, *ts* mutants did not appear to become a predominant variant over a period of up to 42 weeks of cold passaging.

To summarize, cold passaging of RSV 2B and RSV 3A resulted in cold adaptation of virus based on the ability of virus to grow stably at 20°C with consistently high yields. Analysis of EOP assays and the rate of isolation of *ts* mutants indicated that although *ts* mutants did arise in the cold-adapted virus populations, they did not become a predominant species.

### Example 3

#### Screening for Vaccine Candidates in In Vitro Studies

The *ts* mutants were further screened and selected for vaccine candidates based on degree of temperature sensitivity *in vitro*, attenuation in animal models (including mice, cotton rats, and chimps), and retention of neutralizing epitopes.

Over a period of 39 weeks of cold adaptation, a total of 13 RSV 2B and six RSV 3A *ts* mutants were plaque purified a second time and further characterized. Comparison of EOP's at 37/32°C,

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39/32°C, and/or 40/32°C confirmed that these mutants had reduced plaquing efficiency at the higher temperatures and represented a range of temperature sensitivity (see Table 6).

5 Prior to completing the isolation of all 19 mutants described above, a group of four mutants, RSV 2Bp24G, RSV 2Bp20L, RSV 3Ap20E, and RSV 3Ap20F, were selected from the first set of plaque purified viruses for preliminary characterization. To look at actual  
10 virus growth curves, Vero cells were infected with these four mutants at an MOI of 2, and incubated at 20°C, 32°C, 37°C, and 40°C for seven days. The results, shown in Figure 5, indicated that all four mutants were cold-adapted and temperature sensitive, as evidenced by  
15 earlier and higher rises in titer in cultures incubated at 20°C, and reduced or absent growth of virus in cultures incubated at 37°C, 39°C, and 40°C. Based on the degree of temperature sensitivity seen in EOP and growth studies, one subgroup A and one subgroup B  
20 mutant, RSV 2Bp20L and RSV 3Ap20E, were selected to perform additional preliminary experiments on phenotypic stability and growth in mice.

The infectivity and immunogenicity of RSV 2Bp20L and RSV 3Ap20E were evaluated in Balb/c mice.  
25 Virus growth was measured in nasal wash and lung samples harvested four and five days post-infection and serum neutralizing antibody titers were determined 32 days post-infection. Results are shown in Table 7. Growth and immunogenicity of the parental virus was  
30 very low, but detectable. In contrast, no virus was recovered and no neutralizing antibody was detected following inoculation of the *ts* strains, indicating that these strains were highly attenuated in mice.

Of the 19 *ts* mutants which were eventually  
35 isolated, four RSV 2B and three RSV 3A mutants were

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selected for further *in vitro* and *in vivo* characterization. These mutants included the original four mutants described above, as well as three mutants isolated at later time points. Selection criteria  
5 included demonstration of definite *ts* phenotype at both 37°C and 39°C and representation of both subgroups and varying passage strategies and passage numbers. These seven *ts* mutants were plaque purified a third time and amplified to make small working stocks. Their passage  
10 histories are summarized in Table 8. The initial analysis of these mutant strains included comparison of plaquing efficiencies and plaque morphologies at 32°C, 37°C, and 39°C in Vero cells (Table 9), and growth at 32°C, 37°C, 39°C, and 40°C in Vero cells (Table 10). At  
15 37°C and 39°C, EOP was reduced and small and intermediate plaque sizes predominated, indicating that mutants were *ts*. Some breakthrough of "wt" plaque size revertants was seen with all variants except RSV 2Bp34L and RSV 3Ap20F.

20 In growth studies, Vero cells were infected with the virus strains at an MOI of 0.2 and virus yield was determined four days post-infection. Comparison of virus yields in Vero cells at the various temperatures demonstrated that virus yield, expressed as PFU per  
25 cell, decreased significantly at the higher temperatures (37°C, 39°C, 40°C). In some cases, virus yield was also somewhat reduced at 32°C relative to the parental strain, indicating attenuation in growth at 32°C. This is consistent with the smaller plaque sizes  
30 observed in the 32°C EOP assays (Table 9). For all strains, at least one plaque was detected in cells incubated at 39°C or 40°C, suggesting that some revertants were present. Both EOP and virus yield studies demonstrate that these seven isolates possess  
35 varying levels of temperature sensitivity and may

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represent a range of levels of attenuation.

Retention of neutralizing epitopes was examined by comparing reactivities of the seven mutants and parental strains with two neutralizing monoclonal antibodies representing antigenic sites A and C on the F protein described by 19-Beeler and Coelingh (1989) (Table 11). Both antibodies were able to neutralize all the virus strains at similarly high dilutions, indicating that the neutralizing epitopes were intact.

#### Example 4

##### Growth of Mutant Strains in Animal Models

Growth and immunogenicity of the seven ts mutant strains was evaluated in cotton rats. Groups of rats were inoculated intranasally with each mutant and lungs and nasal turbinates were harvested four days post-infection for virus titrations. Sera were collected from an identical set of rats 20 days post-infection to test for neutralizing and EIA antibody responses. A summary of virus titration and immunogenicity results are shown in Table 12. RSV 2B grew well in the nose and lungs, whereas growth of all four RSV 2B ts mutants was very poor. Two of the mutants, RSV 2Bp33F and RSV 2Bp24G, displayed a less attenuated phenotype than did RSV 2Bp20L and RSV 2Bp34L, as indicated by a slightly higher level of replication, as well as a 100% infection rate. The RSV 3A parental and ts mutant strains grew well in the nasal turbinates, but poorly in the lungs. Titers of the RSV 3A ts mutants were lower than that of the parental strain, indicating that the ts mutants were somewhat more attenuated than the parent virus. Neutralizing and EIA-F antibody titers on sera from rats infected with the RSV 2B and RSV 3A parental and ts

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mutant strains were also measured. The level of neutralizing and EIA-F antibody titer was low for the RSV 2B *ts* mutants, consistent with the low level of viral replication seen. Interestingly, titers from animals infected with RSV 2Bp33F were higher than would be expected in view of the low titration values, and may indicate an intermediate level of attenuation for this virus. Neutralizing and EIA-F antibody titrations on all 3 RSV 3A *ts* mutants demonstrated that these mutants were quite immunogenic, consistent with their high level of replication in nasal tissue.

Growth of RSV 2Bp20L was further evaluated in cotton rats from three to seven days post-infection to determine if failure to recover virus was due to a shift in timing of peak titers. RSV 2B was used as a positive control (see Figure 6). The growth kinetics of RSV 2B were typical of other strains of RSV; peak titers occurred on days 4 and 5 in nasal turbinates and on day 4 in lungs. These results substantiate the use of day 4 as the optimal harvest day for the parental strain. RSV 2Bp20L was not detected in lungs and rare plaques were seen in nasal turbinate titrations on days 3, 5, 6, and 7, demonstrating that attenuation of this virus was not simply due to an early or late growth peak.

Relative growth and immunogenicity of RSV 2B and RSV 2Bp20L were also compared in four year old seropositive chimps. Two chimps were infected intranasally with  $10^{4.0}$  and  $10^{5.0}$  PFU of RSV 2B, and two chimps were similarly infected with RSV 2Bp20L. The results are shown in Figure 7 and Table 13. Both chimps infected with RSV 2B developed a mild upper respiratory infection, consisting of nasal discharge and cough. Both chimps shed virus from three through seven days post-infection. The amount of virus shed

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was higher and shedding occurred earlier in the chimp infected with the higher dose of RSV 2B. Neither chimp inoculated with RSV 2Bp20L showed clinical signs of disease or shed virus. Chemistry and hematology workups on all four chimps revealed no significant findings. Serum neutralizing and EIA-F, Ga, and Gb antibody titers were substantially increased 14 and 21 days post-infection with RSV 2B. No rises in antibody titers were seen in chimps inoculated with RSV 2Bp20L. The results indicated that, in seropositive chimps, the parental RSV 2B strain was infectious and immunogenic, whereas the RSV 2Bp20L mutant was highly attenuated.

#### Example 5

##### Challenge Experiments in Cotton Rat Model

Additional experiments were done in cotton rats to evaluate the efficacy of the RSV 2B and 3A ts mutants in preventing infection when challenged with a reference strain of the homologous subgroup (RSV 18537/subgroup B and RSV A2/subgroup A). Cotton rats (eight per group) were inoculated intranasally with each RSV ts mutant. Nasal turbinates and lungs were harvested four days post-infection, from four rats per group, for virus titrations. Six weeks post-infection, the remaining rats were bled for neutralizing and EIA-F titers, then challenged with the appropriate reference RSV strain. Four days post-challenge, nasal turbinates and lungs were removed for virus titration. Results are shown in Tables 14 and 15.

As discussed previously and shown in Table 12, growth of all four RSV 2B TS mutants was very poor compared to the parental RSV 2B strain. Neutralizing



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and EIA antibody titers elicited by RSV 2Bp33F and RSV 2Bp24G were relatively high despite poor virus recovery, possibly indicating an intermediate level of attenuation for both mutants. Level of protection against virus challenge reflected the level of neutralizing antibody response and was high for RSV 2Bp33F and 2Bp24G, moderate for RSV 2Bp20L, and ineffective for RSV 2Bp34L. All RSV 3A strains grew in the nasal turbinates but demonstrated a high level of attenuation in growth in the lungs. Titers of neutralizing and EIA antibodies were high and all rats were completely protected against virus challenge.

The results demonstrate that growth of the attenuated strains elicited protective immunity against virus challenge, suggesting that these strains may be useful as vaccine. Failure of vaccination with the RSV 2Bp34L strain to protect was most likely due to failure of virus to grow due to its high level of attenuation. Since cotton rats are a less susceptible host than humans, failure of this strain to protect does not imply that 2Bp34L would be an ineffective vaccine in humans.

#### Example 6

##### Challenge Experiments in African Green Monkey Model

Growth, immunogenicity, and efficacy of ts mutant strains RSV 2Bp33F, 2Bp24G, 2Bp20L, 3Ap20E, 3Ap20F, and 3Ap28F were evaluated in African green monkeys (AGMs). AGMs are more susceptible to infection with human RSV than are the cotton rats, and characteristics of infection may be more relevant to that seen in humans because of the closer phylogenetic relationship. Two AGMs each were inoculated with  $10^6$  PFU of each mutant virus by combined intranasal and

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intratracheal route. Virus growth was evaluated by nasal wash and bronchial lavage. Neutralizing and EIA antibody responses were tested at approximately 0, 1, 2, 3, 4, 6, and 8 weeks post-infection. Eight weeks post-infection, animals were challenged with  $10^6$  PFU of the parental strain by intranasal and intratracheal route. Virus growth and antibody response was evaluated as described above.

Growth of the parental RSV 2B and 3A strains can be seen in Figures 8 and 9: vaccine controls. Both virus strains grew to high titers in both the nose and lung. Nasal discharge and radiographic evidence of viral pneumonia was seen in one control monkey (032B) infected with RSV 2B, demonstrating that RSV is capable of causing disease in AGMs. These results confirm differences in these characteristics of infection in AGMs vs the cotton rat model, in which disease was not observed and RSV 3A was unable to replicate in the lung. Failure of the parental strains of RSV to cause disease in three of four monkeys suggests that the AGMs are not as susceptible a host as are humans.

Virus titrations for each monkey infected with the RSV 2B ts mutants and then challenged with the parental strain are shown in Figure 8. RSV 2Bp33F grew to low levels in the nasal wash in one of two monkeys, RSV 2Bp24G grew to low levels in nasal wash or in lungs in both monkeys. RSV 2Bp20L failed to grow. In those AGMs where the RSV 2B ts mutants grew, monkeys were partially to fully protected against challenge with parental strain. Tables 16 and 17 give antibody titration results obtained for each monkey post-vaccination (Table 16) and post-virus challenge (Table 17). Results show that in monkeys where virus grew, low levels of neutralizing and EIA antibody titers were seen by 2.5 weeks post-infection. Following challenge

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with the parental strain, antibody titers boosted one full week earlier in vaccinated monkeys with antibody titers prior to challenge, than in vaccinated animals which failed to seroconvert or in unvaccinated controls. This demonstrated that vaccination with these *ts* mutants was sufficient to both prime the immune system and to elicit protection against virus challenge. Because these monkeys are not as susceptible to infection as humans, failure of attenuated virus to grow and to effectively immunize does not imply that virus would not be effective in a fully susceptible host (i.e. seronegative human infant).

Virus growth in AGMs infected with the RSV 3A *ts* mutants and challenged with the parental 3A strain are shown in Figure 9. All three RSV 3A *ts* mutant strains were attenuated in growth, in the order of most to least attenuated: 3Ap28F>3Ap20E>3Ap20F. Vaccination with all three *ts* mutants afforded excellent protection against virus challenge. Antibody response for monkeys vaccinated with RSV 3A *ts* mutants is shown in Table 18, and response following virus challenge is shown in Table 19. In all vaccinated AGMs, with the exception of one monkey given RSV 3Ap28F, low levels of neutralizing and EIA antibody titers were detected beginning three weeks post-vaccination. Following challenge with the parental strain, all vaccinated monkeys boosted a full week earlier than the unvaccinated controls and were protected either fully or partially from infection, demonstrating that vaccination primed the immune response and was protective. This included the one AGM in which antibody response was not detected following vaccination, indicating that measure of serum antibody response may not be fully representative of level of

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protective immunity.

The results from the AGM studies again demonstrate that all six *ts* mutants tested were attenuated. Vaccination with those mutants which were able to replicate in these monkeys was efficacious in preventing infection with challenge virus.

#### Example 7

##### Degree of Attenuation

An RSV *ts* mutant, TS-1, was obtained from Dr. Brian Murphy, NIH. This *ts* mutant was originally derived from the RSV A2 strain by chemical mutagenesis and was tested in clinical trials in seronegative human infants in the 1970's. The outcome of these trials suggested that TS-1 was underattenuated and caused an unacceptable level of disease (rhinitis and otitis media) in infants. In addition, the *ts* phenotype of TS-1 partially reverted following growth in humans. Experiments have been carried out which compare growth of the RSV 2B and 3A *ts* mutants with that of the TS-1 mutant in an attempt to assess the relative *in vivo* attenuation level of the RSV 2A and 3B mutants, and to demonstrate differences between these mutants and what had been used by others in previous clinical trials. The results of the cotton rat study are shown in Table 20, and may be compared directly with the cotton rat data shown in Tables 14 and 15. The TS-1 mutant was less attenuated than the RSV 2B and 3A *ts* mutants, as can most clearly be seen by comparing growth in the lung.

A growth study in African green monkeys (AGMs) comparing TS-1 with RSV 2Bp33F and 3Ap28F was carried out and the results are shown in Figure 10. Monkeys were infected with virus either intranasally

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(TS-1 and 2Bp33F) or intranasally plus intratracheally (3Ap28F). Virus was recovered in one of four monkeys infected with 2Bp33F and two of four monkeys infected with 3Ap28F. Titers were relatively low in both cases, indicating that virus was attenuated. In contrast, relatively high titers of virus were recovered in all four monkeys inoculated with TS-1. In two of four monkeys, the levels of TS-1 titers were equivalent to those seen in monkeys infected with wild type virus. TS-1 did not spread to the lungs, as would be expected for wild type virus, indicating that TS-1 was somewhat attenuated. The results clearly show that RSV 2Bp33F and 3Ap28F have different phenotypic characteristics than TS-1 and are significantly more attenuated. This higher level of attenuation is a property that is desirable for a vaccine to be administered to human infants.

#### Example 8

##### Sequence Analyses of RSV Subgroup B Strains

The temperature-sensitive (*ts*) phenotype is strongly associated with attenuation *in vivo*; in addition, some non-*ts* mutations may also be attenuating. Identification of *ts* and non-*ts* attenuating mutations was achieved by sequence analysis and evaluation of *ts*, cold-adapted (*ca*), and *in vivo* growth phenotypes of RSV mutants and revertants.

The genomes of the following five RSV 2B strains have now been completely sequenced: 2B parent, 2B33F, one revertant designated 2B33F TS(+), 2B20L and one revertant designated 2B20L TS(+). The 2B33F and 2B20L strains are *ts* and *ca* and are described in U.S. Serial No. 08/059,444 (78), which is hereby incorporated by reference. After identifying regions

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where mutations in 2B33F and 2B20L are located, nine additional isolates of 2B33F "revertants" obtained following *in vitro* passaging at 39°C and *in vivo* passaging in African Green Monkeys or chimpanzees, and nine additional isolates of 2B20L "revertants" obtained following *in vitro* passaging at 39°C have been sequenced in those regions. The *ts*, *ca*, and attenuation phenotypes of many of these revertants have now been characterized and assessed. Correlations between phenotype *ts*, vaccine attenuation and sequence changes have been identified.

A summary of results is presented in Tables 21-26.

Several significant observations can be drawn from these data:

a. As shown in Tables 21 (for 2B33F) and 22 (for 2B20L), there are relatively few sequence changes identified in the two mutant strains: RSV 2B33F differs from parental RSV 2B by two changes at the 3' genomic promoter region, two changes at the non-coding 5'-end of the M gene, and four coding changes plus one non-coding (poly(A) motif) change in the RNA dependent RNA polymerase coding L gene. In addition, 14 changes mapped to the SH gene alone. RSV 2B20L differs from its RSV 2B parent only at seven nucleotide positions, of which three are common with 2B33F virus, including two changes at the 3' genomic promoter and one coding change in the L gene. Two additional unique changes of 2B20L virus mapped to the coding region of the L gene. Potentially attenuating mutations at the RNA dependent RNA polymerase gene have been identified.

b. Two *ts* mutations can be identified in the L gene of the attenuated virus strains 2B33F and 2B20L:

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(i) In 2B33F, a mutation at nucleotide position 9853 (A → G) leading to a coding change in L protein at amino acid 451 (Lys → Arg) is clearly associated with the *ts* and attenuation phenotypes. Reversion at this site alone in the 2B33F TS(+) 5a strain is responsible for complete restoration of growth at 39°C (Table 23) and partial reversion in attenuation in animals. This association of *ts* was also supported by partial sequence analyses of six additional "full *ts* revertants" (designated 4a, 3b, pp2, 3A, 5a, 5A) isolated from cell culture and from chimps, in which only the nucleotide 9853 mutation reverted (Tables 24-26) (note that one AGM (African Green Monkey) isolate which reverted at 9853 only partially reverted in *ts* phenotype). This amino acid 451 mutation (Lys → Arg) is amenable to stabilization in cDNA infectious clone constructs, by inserting a second mutation to stabilize the codon, thereby lessening the likelihood that it will revert back to Lys.

(ii) In 2B20L, a mutation at base 14,649 (A → G) leading to a coding change in the L protein (amino acid position 2,050, Asn → Asp) appears to be associated with the *ts* and attenuation phenotypes. This aspartic acid at the amino acid 2050 invariably reverts back (Asp → Asn) in TS(+) revertants or changes to a different amino acid (Asp → Val) by nucleotide substitution at position 14,650 (A → T) (Tables 22, 25). The above observation is based on complete sequence analysis on the TS(+) revertant R1 and partial sequence of several additional TS(+) revertants (R2, R4A, R7A, R8A) at selected regions (Table 25). An

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additional mutation is seen in the R1 revertant at nucleotide position 13,347 (amino acid 1616, Asn → Asp) associated with the above reversion. However, the effect of this mutation on the *ts* phenotype is not known; the L gene of other revertants has not been sequenced completely.

c. Three base changes are common to 2B33F and 2B20L strains of virus:

(i) A change at position 14,587 (C → T) with a corresponding change (Thr → Ile) at amino acid 2029 is present in both 2B33F and 2B20L (Tables 21,22). This nucleotide "T" substitution was found to be present in 10% of the population of the progenitor RSV2B strain and may have been preferred during the attenuation process. No wildtype base "C" was found in the 2B33F and 2B20L virus.

(ii) Two mutations are seen in the 2B33F and 2B20L 3' genomic promoter region: nucleotide 4 (C → G) and the insertion of an extra A in the stretch of A's at positions 6-11 (in antigenomic, message sense). When the sequences of selected TS(+) revertants were analyzed, these mutations were seen to have been retained in the 2B33F TS(+)5a (Table 21) and the 2B20L TS(+)R1 (Table 22) revertants. These non-coding, cis-acting mutations remained associated with partial viral attenuation.

Expression using the minireplicon RSV-CAT system for the analysis of these cis-acting changes has shown the 3' genomic promoter nucleotide 4 (C → G) change to be an upregulation of transcription/replication in this *in vitro* system when



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the 2B progenitor virus or either of the 2B33F or 2B33F TS(+) provided helper L gene functions (the N, P and M2 genes are identical in these viruses).

Complementation analysis of the 2B33F 3' genomic promoter and the helper functions provided by the progenitor RSV2B virus or the 2B33F and 2B33F TS(+) viruses by this RSV-CAT minireplicon system has also been conducted. All three viruses supported both the 2B and 2B33F 3' genomic promoter mediated transcription/replication functions. However, the 2B33F and 2B33F TS(+) viruses preferred their 2B33F 3' genomic promoters. This analysis clearly shows co-evolution of 3' genomic promoter changes during the vaccine attenuation process, along with the RNA dependent RNA polymerase gene. Reversion of *ts* phenotype in the 2B33F mutant 5a by reversion of the single L protein amino acid 451 (Arg → Lys) by sequence analysis was clearly demonstrated by support of transcription/replication functions of RSV-CAT minireplicon at 37°C. The 2B33F virus did not provide helper functions to the RSV-CAT minireplicon (with 2B or 2B33F 3' genomic promoters) at 37°C.

d. A biased hypermutation of SH seen in 2B33F is present in all 2B33F revertants, regardless of phenotype, and is not seen in 2B20L, which is *ts*, *ca*, and attenuated. Thus, there are no data at this time that associate this mutation with any biological phenotype.

Another wild-type RSV designated 18537 was also sequenced and compared to the sequence of the wild-type RSV 2B strain. With one exception, at all the critical residues described above, the two wild-type strains were identical. For 2B, the codon ACA at nucleotides 14586-14588 encodes a Thr at amino acid

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2029 of the L protein, while for 18537, the codon ATT at nucleotides 14593-14595 encodes an Ile at amino acid 2029 (the L gene start codon is at nucleotides 8509-8511 in 18537, compared to 8502-8504 in 2B).

5

#### Example 9

##### PCR Assay to Detect RSV

10 A PCR assay is used to detect the presence of RSV. PCR primers are designed and selected based on homologies to the RSV sequences described herein to be specific for all subgroup B strains, or for the individual wild-type, vaccine or revertant RSV subgroup B strains described herein. The assay is conducted by  
15 subjecting the sample to reverse transcription of RNA, followed by PCR amplification of selected cDNA regions corresponding to RSV nucleotide sequence. Amplified PCR products are identified on gels and their specificity confirmed by hybridization with specific  
20 RSV nucleotide probes.

#### Example 10

##### ELISA to Detect RSV

25 An ELISA test is used to detect the presence of RSV. Peptides are designed and selected based on homologies to the RSV sequences described herein to be specific for all subgroup B strains, or for individual wild-type, vaccine or revertant RSV subgroup B strains  
30 described herein. These peptides are then coupled to KLH and used to immunize rabbits for the production of monospecific polyclonal antibody. A selection of these polyclonal antibodies, or a combination of polyclonal and monoclonal antibodies is then used in a "capture  
35 ELISA" to detect the presence of an RSV antigen.

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Table 1  
RSV 2B Cold Adaptation

Passage #	Cumm. Time Passage Weeks	E, F		Virus Yield	
		<u>Incubation</u>		<u>log<sub>10</sub> PFU</u>	
		Temp °C	Time Days	E	F
1	0.2	26	2	6.9	6.7
2	0.4	26	2	6.0	6.1
3	0.6	26	2	5.5	5.6
4	0.8	26	2	4.5	4.7
5	1.0	26	7	4.9	5.0
6	2.0	26	7	6.2	6.3
7	3.0	26	7	7.9*	7.6*
8	4.0	22	7	7.5	7.6
9	5.0	22	7	7.3	7.3
10	6.0	22	7	7.2*	7.2*
11	7.0	22	7	7.5*	7.7*
12	8.0	22	7	8.0*	7.9*
13	9.0	22	7	8.0*	7.9*
14	10.0	20	7	7.6	7.7
15	11.0	20	7	7.0	5.9
16	12.0	20	7	7.2	7.1
17	13.0	20	7	6.7	6.3
18	15.0	20	14	5.5	5.2
19	17.0	20	14	6.3	6.0
20	18.0	20	7	6.1	5.8
21	19.0	20	7	5.4	5.7
22	20.0	20	7	5.9	5.7
23	21.0	20	7	6.3	5.5
24	22.0	20	7	6.9	6.3
25	23.0	20	7	6.8	6.6
26	24.0	20	8	6.6	6.2
27	25.0	20	7	6.3	6.0
28	26.0	20	6	6.5	6.2
29	27.0	20	7	6.2	6.3
30	28.0	20	7	7.0	7.2
31	29.0	20	7	7.3	7.1
32	30.0	20	7	6.8	6.5
33	31.0	20	7	6.9	6.7
34	32.0	20	7	6.9	7.0
35	33.0	20	7	7.4	7.0
36	34.0	20	7	7.2	7.1
37	35.0	20	7	7.4	7.0
38	36.0	20	7	7.4	7.1
39	37.0	20	7	7.5	7.0
40	38.0	20	7	7.2	6.7

\*Syncytial CPE seen at harvest

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Table 1b  
RSV 2B Cold Adaptation

Passage #	Cumm. Time Passage Weeks	G,H		Virus Yield	
		Temp °C	Time Days	log <sub>10</sub> PFU	
				G	H
1	0.3	26	3	7.1	7.1
2	0.7	26	3	6.9	6.9
3	1.0	22	7	6.4	6.4
4	2.0	22	7	6.4	6.3
5	3.0	22	7	6.6	6.4
6	4.0	22	7	6.9	6.8
7	5.0	20	7	6.9	6.7
8	6.0	20	7	6.3	6.3
9	7.0	20	7	6.2	6.3
10	8.0	20	7	6.6	6.9
11	9.0	20	7	7.0	7.0
12	10.0	20	7	7.0	7.4
13	11.0	20	7	6.3	7.3
14	12.0	20	7	7.7	7.9
15	13.0	20	7	7.2	7.4
16	15.0	20	14	6.4	6.3
17	16.0	20	8	6.8	6.9
18	17.0	20	6	6.9	7.0
19	18.0	20	7	6.9	7.1
20	19.0	20	7	6.7	7.0
21	20.0	20	7	6.4	6.8
22	21.0	20	7	6.5	7.0
23	22.0	20	7	6.9	7.1
24	23.0	20	7	6.8	6.7
25	24.0	20	8	6.4	6.2
26	25.0	20	7	6.0	5.5
27	26.0	20	6	6.3	5.5
28	27.0	20	7	6.5	5.9
29	28.0	20	7	7.1	6.4
30	29.0	20	7	6.1	7.1
31	30.0	20	7	6.4	5.5
32	31.0	20	7	6.2	5.9
33	32.0	20	7	6.4	6.2
34	33.0	20	7	6.4	6.9
35	34.0	20	7	6.9	6.5
36	35.0	20	7	7.0	6.7
38	37.0	20	7	7.1	7.2

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Table 1c  
RSV 2B Cold Adaptation

Passage #	Cumm. Time Passage Weeks	J, L		Virus Yield	
		Temp °C	Time Days	log <sub>10</sub> PFU	
				J	L
1	1.0	22	7	6.8	
2	2.0	22	7	7.1	
3	3.0	22	7	6.7	
4	4.0	22	7	5.9	6.1
5	5.0	22	7	4.8	5.7
6	6.0	20	7	4.9	5.0
7	7.0	20	7	4.8	4.9
8	9.0	20	14	6.0	6.0
9	11.0	20	14	6.6	6.3
10	12.0	20	7	6.9	6.9
11	13.0	20	7	6.6	6.7
12	15.0	20	14	6.0	6.0
13	16.0	20	8	6.3	6.2
14	17.0	20	6	6.2	6.5
15	18.0	20	7	6.6	6.7
16	19.0	20	7	6.4	6.9
17	20.0	20	7	6.5	6.9
18	21.0	20	7	6.9	7.0
19	22.0	20	7	7.4	7.4
20	23.0	20	7	7.2	7.4
21	24.0	20	8	7.0	7.1
22	25.0	20	7	6.8	6.9
23	26.0	20	6	6.9	7.0
24	27.0	20	7	7.0	7.0
25	28.0	20	7	7.8	7.4
26	29.0	20	7	7.5	7.3
27	30.0	20	7	6.8	6.7
28	31.0	20	7	6.9	6.8
29	32.0	20	7	7.0	6.9
30	33.0	20	7	7.4	7.2
31	34.0	20	7	7.3	6.7
32	35.0	20	7	7.3	6.9
33	36.0	20	7	7.3	7.0
34	37.0	20	7	7.2	6.9
35	38.0	20	7	6.6	6.3

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Table 2a  
RSV 3A Cold Adaptation

E				
Passage #	Cumm. Time	Incubation	Virus Yield	
	Passage	Temp	Time	$\log_{10}$ PFU
	Weeks	°C	Days	E
1	0.2	26	2	6.2
2	0.4	26	2	5.1
3	0.6	26	2	4.7
4	0.8	26	2	3.8
5	1.0	26	7	4.0
6	2.0	26	7	5.0
7	3.0	26	7	6.1
8	4.0	22	7	6.0
9	5.0	22	7	5.6
10	6.0	22	7	5.8
11	7.0	22	7	5.7
12	8.0	22	7	5.9
13	9.0	22	7	5.9
14	11.0	20	14	5.8
15	13.0	20	14	6.1
16	15.0	20	14	4.8
17	17.0	20	14	4.9
18	19.0	20	14	4.8
19	20.0	20	7	4.3
20	22.0	20	14	4.9
21	24.0	20	14	5.2
22	26.0	20	15	5.6
23	28.0	20	13	6.3
24	30.0	20	14	6.3
25	32.0	20	14	7.3
26	34.0	20	14	7.8
27	36.0	20	14	7.2
28	38.0	20	14	7.4
29	40.0	20	14	6.8
30	42.0	20	14	7.3

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Table 2b  
RSV 3A Cold Adaptation

F				
	Cumm. Time	Incubation		Virus Yield
Passage	Passage	Temp	Time	$\log_{10}$ PFU
<u>#</u>	<u>Weeks</u>	<u>°C</u>	<u>Days</u>	<u>F</u>
1	0.2	26	2	6.1
2	0.4	26	2	5.1
3	0.6	26	2	4.7
4	0.8	26	2	3.6
5	1.0	26	7	4.3
6	2.0	26	7	5.3
7	3.0	26	7	6.4
8	4.0	22	7	6.3
9	5.0	22	7	5.2
10	6.0	22	7	5.8
11	7.0	22	7	5.7
12	8.0	22	7	6.0
13	9.0	22	7	5.6
14	11.0	20	14	5.5
15	13.0	20	14	5.4
16	15.0	20	14	3.9
17	17.0	20	14	3.7
18	19.0	20	14	3.5
19	21.0	20	14	3.8
20	23.0	20	14	4.2
21	25.0	20	15	3.2
22	27.0	20	13	3.9
23	29.0	20	14	4.5
24	31.0	20	14	4.7
25	33.0	20	14	4.8
26	35.0	20	14	5.3
27	37.0	20	14	5.5
28	39.0	20	14	5.8

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Table 2c  
RSV 3A Cold Adaptation

Passage #	Cumm. Time Passage Weeks	H, I		Virus Yield	
		Incubation		log <sub>10</sub> PFU	
		Temp °C	Time Days	H	I
1	0.3	26	3	6.9	7.0
2	0.7	26	3	6.1	6.4
3	1.0	22	7	5.8	5.8
4	2.0	22	7	5.8	5.9
5	3.0	22	7	5.9	5.7
6	4.0	22	7	5.6	5.5
7	5.0	22	7	5.1	5.1
8	6.0	20	7	4.0	3.8
9	7.0	20	7	3.3	2.8
10	9.0	20	14	3.9	3.2
11	11.0	20	14	3.9	3.1
12	13.0	20	14	4.0	3.0

Passage #	Cumm. Time Passage Weeks	J, L		Virus Yield	
		Incubation		log <sub>10</sub> PFU	
		Temp °C	Time Days	J	L
1	1.0	22	7	6.7	
2	2.0	22	7	6.7	
3	3.0	22	7	6.0	
4	4.0	22	7	5.7	5.6
5	5.0	22	7	4.2	4.9
6	6.0	20	7	3.7	3.7
7	7.0	20	7	3.1	3.0
8	9.0	20	14	2.8	3.2
9	11.0	20	14	2.3	3.3
10	13.0	20	14	3.0	2.8



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Table 3  
Summary of Cold Adaptation Passage History

<u>#Parental Virus Passage</u>					<u># Cold Adaptation Passage</u>				
<u>PRMK      Vero</u>					<u>Vero</u>				
<u>Virus</u>	<u>35°C</u>	<u>35°C</u>	<u>36°C</u>	<u>Total</u>	<u>Flask</u>	<u>26°C</u>	<u>22°C</u>	<u>20°C</u>	<u>Total</u>
2B	7	2	12	21	E, F	7	6	27	40
					G, H	2	5	32	39
					J, L	0	5	30	35
3A	8	2	12	22	E	7	6	17	30
					F	7	6	15	28
					H, I	2	5	5	12
					J, L	0	5	5	10

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Table 4  
Efficiency of Plaquing of Cold Passaged Virus

<u>Virus</u>	<u>Week 5</u>	<u>Week 17</u>
2B	0.8	0.6
2B-E	0.6	0.6
2B-F	0.8	0.7
2B-G	0.6	0.8
2B-H	0.7	0.4
2B-J	ND	0.9
2B-L	0.7	0.6
3A	0.6	0.6
3A-E	0.6	0.4
3A-F	0.8	0.2
3A-H	0.6	ND
3A-I	0.9	ND
3A-J	0.6	ND
3A-L	0.6	ND

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Table 5

## TS Mutants Plaque Purified from Cold Adapted Virus

Cumm./Passage Weeks      #	#TS/#Total Plaques <u>Isolated</u>		Cumm./Passage Weeks      #	#TS/#Total Plaques <u>Isolated</u>	
	<u>E</u>	<u>F</u>		<u>E</u>	
wk23/p25	0/10	1/10	wk22/p20	2/10	
wk31/p33	0/10	1/10	wk32/p25	1/10	
wk38/p40	0/10	1/10	wk42/p30	3/9	
	<u>G</u>	<u>H</u>		<u>F</u>	
wk23/p24	1/10	2/10	wk23/p20	1/9	
wk31/p32	0/10	2/10	wk31/p24	0/10	
wk38/p39	1/10	4/10	wk37/p27	1/10	
	<u>J</u>	<u>L</u>	wk39/p28	2/5	
wk23/p20	0/9	1/10			
wk31/p28	0/10	0/10			
wk37/p34	0/8	2/9			
wk38/p35	1/20	3/8			

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Table 6

Summary of EOP Data on Twice  
Plaque Purified RSV TS Mutants

<u>RSV Isolate</u>	<u>EOP</u>		
	<u>37/32°C</u>	<u>39/32°C</u>	<u>40/32°C</u>
2B (parent)	0.7-1.0	0.6-0.8	0.4
2Bp33F (pp10-1)	0.5	0.002	ND
2Bp40F (pp7-2)		0.0008	ND
2Bp24G (pp2-1)	0.2	0.00001	<0.00001
2Bp39G (pp7-3)	1.0	0.009	ND
2Bp24H (pp3-2)	ND	0.003	0.001
2Bp32H (pp6-2)	0.9	0.03	ND
2Bp39H (pp6-5)	1.0	0.04	ND
2Bp35J (pp2-1)	0.4	0.2	ND
2Bp20L (pp5-1)	0.02	ND	<0.00001
2Bp34L (pp2-2)	0.005	0.0005	ND
2Bp35L (pp1-1)	0.3	0.02	ND
2Bp35L (pp2-1)	0.5	0.1	ND
2Bp35L (pp8-3)	0.2	0.05	ND

<u>RSV Isolate</u>	<u>EOP</u>		
	<u>37/32°C</u>	<u>39/32°C</u>	<u>40/32°C</u>
3B (parent)	1.0	0.5-0.9	0.6
3Ap20E (pp3-1)	0.6	0.006	0.000009
3Ap25E (pp7-5)	0.5	0.2	ND
3Ap30E (pp3-1)	0.4	0.08	
3Ap20F (pp4-3)	0.8	>0.1	0.000004
3Ap27F (pp1-2)	0.3	0.003	ND
3Ap28F (pp10-1)	0.2	0.002	ND

ND = Not Done

Table 7  
RSV Infection of BALB/c Mice: Attenuation and Immunogenicity

Virus Strain	Dose $\log_{10}$ PFU	Infection Rate	Nasal Wash $\log_{10}$ PFU/ml		Lung Tissue $\log_{10}$ PFU/g		Antibody Titers*		
			day 4	day 5	day 4	day 5	2B	3A	A2
2B (parental)	6.2	8/8+	2.0	1.9	2.8	2.0*	17	21	<8
2B-CAP20L	6.3	0/8	N.P.	N.P.	N.P.	N.P.	<8	<8	<8
3A (parental)	6.0	8/8	1.4	0.5*	2.3*	2.6	19	57	11
3A-Cap-20E	6.5	0/8	N.P.	N.P.	N.P.	N.P.	<8	<8	<8
Vero	---	0/8	N.P.	N.P.	N.P.	N.P.	<8	<8	<8

N.P. = No plaques

\* = Values are below optimal detection limits of assay based on a minimum of 1 plaque per well.

+ = Sera was taken 32 days post-infection.

Neutralization results are expressed as the reciprocal of the dilution giving 60% plaque reduction neutralization, again RSV 2B, 3A, and A2

F = Infection rate = # of mice positive for RSV/Total # of mice inoculated.

Table 8  
Summary of RSV TS Mutant Passage History

	# Vero Passage							
	<u>PRMK</u>	Adaptation and Plaque		Cold Adaptation			Plaque Purification (x3) + expansion	
		Purification (x3) (parental virus)	35°C	36°C	26°C	22°C		20°C
<u>Virus</u>	<u>35°C</u>							
2Bp33F pp10-1-2	7	2	12	7	6	20	6	
2Bp24G pp2-1-1	7	2	12	2	5	17	5	
2Bp20L pp5-1-1	7	2	12	-	5	15	5	
2Bp34L pp2-2-2	7	2	12	-	5	29	5	
3Ap20E pp3-1-1	8	2	12	7	6	7	5	
3Ap20F pp4-3-1	8	2	12	7	6	7	5	
3Ap28F pp10-1-2	8	2	12	7	6	15	5	

Table 9  
EOP and Plaque Morphology of RSV 2B and RSV 3A TS Mutants in Vero Cells

<u>VIRUS</u>	<u>TEMPERATURE</u> (°C)	<u>EOP</u>	<u>PLAQUE MORPHOLOGY</u> <u>OBSERVATIONS</u>
2B	32°	1.0	99% WT
	37°	0.9	H, Most WT
	39°	0.6	99% WT
2Bp33F	32°	1.0	1/3 SP, I, WT
pp10-1-2, V+3	37°	0.01	Mostly SP, F
	39°	0.00005	95% SP, D, Few WT
2Bp24G	32°	1.0	1/3 SP, I, WT
pp2-1-1, V+3	37°	0.09	H, SP and I
	39°	0.004	1/3 SP, I, WT
2Bp20L	32°	1.0	H, 1/3 WT
pp5-1-1, V+4	37°	0.01	1/3, SP, I, WT
0.0002	39°	0.0002	1/3 SP, I, WT
2Bp34L	32°	1.0	H, Mostly I
pp2-2-2, V+3	37°	0.002	Mostly SP, F
	39°	0.0001	Very SP, No WT

Table 9 (continued)  
EOP and Plaque Morphology of RSV 2B and RSV 3A TS Mutants in Vero Cells

<u>VIRUS</u>	<u>TEMPERATURE</u> (°C)	<u>EOP</u>	<u>PLAQUE MORPHOLOGY</u> <u>OBSERVATIONS</u>
3A	32°	1.0	99% WT
	37°	0.9	Mostly WT
	39°	0.5	Mostly WT
3Ap20E pp3-1-1, V+4	32°	1.0	Mostly I
	37°	0.8	Mostly I, 1/3 SP
	39°	0.04	95% SP, I, F, Few WT
3Ap20F pp4-3-1, V+3	32°	1.0	Mostly I and WT
	37°	0.7	Mostly I and WT
	39°	0.1	Mostly SP, I, No WT
3Ap23F pp10-1-2, V+3	32°	1.0	Mostly SP and I
	37°	0.4	Mostly I, F, Few WT
	39°	0.01	90% SP, I, F, Few WT

\*\*\*\*\*

Abbreviations: SP Small Plaque  
I Intermediate  
WT Wild Type  
D Dark Stained  
F Faint Stained  
H Heterogeneous



Table 10  
Temperature-Related Growth of RSV 2B and 3A strains  
in Vero Cells: Four Day Virus Yields

Virus	Virus Yield			
	PFU/Cell 32°C	37°C	39°C	40°C
2B	0.8	0.6	0.4	0.1
2BP33F pp10-1-2, V+3	0.5	0.01	≤0.00008	<0.000005
2BP24G pp2-1-1, V+3	1.0	0.08	0.0003	0.00001
2BP20L pp5-1-1, V+4	0.5	0.01	0.00003	0.000007
2BP34L pp2-2-2, V+3	0.008	<0.000005	<0.000005	≤0.000007
3A	1.6	0.3	0.08	0.05
3Ap20E pp3-1-1, V+4	0.2	0.02	≤0.000006	<0.000006
3Ap20F pp1-3-1, V+3	0.5	0.05	0.00005	<0.000006
3Ap28F pp10-1-2, V+3	0.2	0.006	≤0.000006	<0.000006

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Table 11  
 Monoclonal Antibody Neutralization of  
 RSV 2B and RSV 3A Parental and TS Mutants

<u>Challenge Strains</u>	<u>Neutralization Titers</u>	
	<u>143-6C</u>	<u>133-1H</u>
2B	15,091	46,775
2Bp33F	23,364	32,690
2Bp24G	>25,600	32,571
2Bp20L	25,972	32,790
2Bp34L	16,757	77,172
3A	99,814	46,493
3Ap20E	76,203	>25,600
3Ap20F	69,513	13,743
3Ap28F	80,436	34,136

Neutralizations were done by a standard 60% plaque reduction neutralization assay on Vero cell monolayers in 96-well microtiter plates. Challenge with a 1:400 dilution of non-neutralizing monoclonal antibody 131-2G showed no reduction in titer in any of the nine strains.

Table 12  
RSV TS Mutant Infection of Cotton Rats - 4 Days Post-Infection

Immunogenicity*										Virus Growth		
Virus Strain	Dose Log <sub>10</sub> Pfu	Infection Rate	Log <sub>10</sub> Nasal	GMT+ PFU/gm Lung	Sero(+) Rate	Challenge Virus			EIA-F	EIA-Ga	EIA-Gb	
						RSV 28	RSV A2	RSV 3A				
2B	6.5	4/4	5.48 (0.19)	5.00 (0.42)	4/4	2.80 (0.36)	2.26 (.052)	3.42 (0.40)	3.43 (0.14)	<1.95 (0.30)	3.23 (0.13)	
2Bp33F	7.3	4/4	1.88 (.028)	<1.30 (0.12)	4/4	2.24 (0.22)	1.86 (0.48)	2.95 (0.25)	2.76 (0.26)	<1.70	2.33 (0.25)	
2Bp24G	6.9	4/4	1.73 (0.33)	<1.30 (0.08)	4/4	1.58 (0.23)	<1.05 (0.05)	2.33 (0.24)	2.62 (0.34)	<1.71 (0.01)	2.10 (0.32)	
2Bp20L	7.0	0/4	<1.92 (0.11)	<1.30 (0.12)	2/3	<1.26 (0.24)	<1.01 (0.02)	<1.25 (0.31)	<2.05 (0.32)	<1.70	<1.70	
2Bp34L	5.6	1/4	<1.73 (0.05)	<1.33 (0.10)	1/3	<1.03 (0.06)	<1.00	<1.08 (0.08)	<1.70	<1.70	<1.70	
3A	6.3	4/4	5.70 (0.23)	2.00 (0.42)	4/4	2.31 (0.13)	2.28 (0.28)	3.12 (0.31)	3.55 (0.18)	2.28 (0.29)	<1.93 (0.46)	
3Ap20E	6.5	4/4	4.97 (0.22)	<1.40 (0.22)	4/4	2.09 (0.05)	1.74 (0.09)	2.59 (0.16)	3.40 (0.18)	2.61 (0.58)	2.18 (0.32)	
3Ap20F	6.7	4/4	4.95 (0.13)	<1.70 (0.29)	4/4	2.40 (0.41)	2.59 (0.26)	3.32 (0.39)	3.62 (0.12)	2.88 (0.33)	2.57 (0.47)	
3Ap28F	6.4	4/4	3.98 (0.86)	<1.40 (0.05)	4/4	2.12 (0.64)	1.90 (0.44)	2.73 (0.36)	3.28 (0.36)	2.45 (0.16)	<1.83 (0.22)	

+ GMT = geometric mean titer

\* Sera obtained from animals three weeks post-infection.

PRINT is a 60% plaque reduction neutralization test.

EIA-F, Ga, Gb are enzyme immunoassays testing reactivity of sera with purified F protein (from RSV A2), purified Ga (from RSV A2, and purified Gb (from RSV 18537).

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Table 13  
RSV Infection of Seropositive Chimps

<u>VIRUS</u>	<u>DOSE</u>	<u>DAY</u>	<u>NEUTRALIZATION TITERS<sup>1</sup></u> (LOG <sub>10</sub> )				<u>EIA TITERS<sup>2</sup></u> (LOG <sub>10</sub> )			
			<u>2B</u>	<u>3A</u>	<u>A2</u>	<u>ETA-F</u>	<u>EIA-Ga</u>	<u>EIA-Gb</u>	<u>EIA-Ga</u>	<u>EIA-Gb</u>
RSV 2B	4.0 PFU	-1	2.0	2.1	2.0	4.1	3.6	2.9	3.6	2.9
		7	2.7	2.4	2.4	4.2	3.4	3.1	3.4	3.1
		14	5.0	5.1	5.0	6.6	5.4	5.2	5.4	5.2
		21	4.9	5.0	4.9	6.5	5.3	5.2	5.3	5.2
		D21/D-1*	2.9	2.9	2.9	2.4	1.7	2.3	1.7	2.3
RSV2B	5.0 PFU	-1	2.4	2.8	2.8	4.6	4.3	3.5	4.3	3.5
		7	2.9	3.2	3.0	4.9	4.3	3.5	4.3	3.5
		14	5.0	5.1	>5.1	6.5	5.5	4.7	5.5	4.7
		21	4.8	5.4	4.9	6.4	5.8	5.3	5.8	5.3
		D21/D-1	2.4	2.6	2.1	1.8	1.5	1.8	1.5	1.8
RSV 2Bp20L	4.0 PFU	-1	2.1	2.7	2.1	4.2	3.7	2.7	3.7	2.7
		7	2.2	2.4	2.0	4.2	3.8	2.6	3.8	2.6
		14	2.0	2.4	1.9	4.1	3.8	2.6	3.8	2.6
		21	2.2	2.8	2.4	4.1	3.7	2.8	3.7	2.8
		D21/D-1	0.1	0.1	0.3	-0.1	0.0	0.1	0.0	0.1
RSV 2Bp20L	5.0 PFU	-1	1.8	2.6	2.3	3.8	4.0	3.0	4.0	3.0
		7	1.8	2.2	2.2	3.7	3.9	2.8	3.9	2.8
		14	2.2	2.5	1.9	3.8	3.9	2.7	3.9	2.7
		21	2.4	2.5	2.1	3.9	4.0	3.0	4.0	3.0
		D21/D-1	0.6	-0.1	-0.2	0.1	0.0	0.0	0.0	0.0

SUBSTITUTE SHEET (RULE 26)

1 = 60% plaque reduction neutralization assay performed against RSV strain 2B, 3A, + A2.

2 = Enzyme immunoassay testing reactivity purified RSV.

Source of protein = F(RSV A2), Ga(RSV A2), Gb(RSV 18537).

\* Rise in titer day - 1 to day 21.

Table 14  
Growth, Immunogenicity, and Efficacy of RSV 2B ts Mutants in Cotton Rats<sup>1</sup>

Virus	Dose	Virus Titer (log <sub>10</sub> PFU/gm)			Immunogenicity <sup>2</sup>			Challenge Virus Titer (log <sub>10</sub> PFU/gm)		
		#RSV+	Nose	Lung	Neutralization			#RSV+	Nose	Lung
					A2	3A	2B	EIA-F <sup>2</sup>		
2B	6.1	4/4	≤3.1	4.6	174	502	521	1911	1/3	≤2.0
2Bp33F	5.8	2/4	≤1.2	<1.1	35	115	145	1041	1/4	<1.8
2Bp24G	6.4	2/4	≤1.3	≤1.0	92	201	377	2432	0/4	<1.7
2Bp20L	6.2	0/4	<1.3	<1.0	41	123	75	482	3/4	≤2.6
2Bp34L	5.2	0/4	<1.3	<1.1	<10	<10	<10	≤77	4/4	4.8
PBS					<10	<10	<10	<50	4/4	4.9
										5.5

1 = Cotton rats were inoculated with virus by intranasal route. Four days post-infection, lungs and nasal turbinates were harvested for virus titrations. Six weeks post-infection, blood was taken for neutralization and EIA titrations and rats were challenged intranasally with 10<sup>6</sup> PFU of RSV 18537. Lungs and nasal turbinates were harvested 4 days post-challenge. Virus and antibody titers are reported as geometric mean titers.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

Table 15  
Growth, Immunogenicity, and Efficacy of RSV 3A ts Mutants in Cotton Rats<sup>1</sup>

Virus	Dose	Virus Titer			Immunogenicity				Challenge Virus Titer		
		(log <sub>10</sub> PFU/gm)			Neutralization <sup>2</sup>				(log <sub>10</sub> PFU/gm)		
		#RSV+	Nose	Lung	A <sub>2</sub>	3A	2B	EIA-F <sup>2</sup>	#RSV+	Nose	Lung
3A	6.0	4/4	3.2	<4.1	35	141	35	1202	0/3	<1.6	<1.4
3Ap20E	6.0	4/4	≤3.2	≤1.4	≤17	85	66	646	0/4	<1.6	<1.3
3Ap20F	6.0	4/4	3.7	<1.3	≤23	87	55	708	0/4	<1.8	<1.2
3Ap28F	6.0	3/4	≤2.3	<1.4	47	282	123	2188	0/4	<1.6	<1.4
PBS					<10	<10	<10	<50	4/4	5.6	5.6

1 = Cotton rats were inoculated with virus by intranasal route. Four days post-infection, lungs and nasal turbinates were harvested for virus titrations. Six weeks post-infection, blood was taken for neutralization and EIA titrations and rats were challenged intranasally with 10<sup>6</sup> PFU of RSV A2.

Lungs and nasal turbinates were harvested 4 days post-challenge. Virus and antibody titers are reported as geometric mean titers.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 16  
RSV Growth and Immunogenicity in African Green Monkeys:  
RSV 2B ts Mutants<sup>1</sup>

		<u>ts Mutant</u>		<u>Immunogenicity</u>				
		<u>Virus Growth</u>		<u>Day</u>	<u>Neutralization</u>			<u>EIA</u>
		<u>Peak Virus Titer</u>			<u>Titers<sup>2</sup></u>			<u>Titers<sup>3</sup></u>
<u>Virus</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>					<u>(x10<sup>3</sup>)</u>
								<u>anti-F</u>
2Bp33F	SK034	<0.7	<0.7	0	<10	<10	<10	<0.15
				7	<10	<10	<10	<0.15
				14	<10	<10	<10	0.88
				24	<10	<10	<10	0.49
				27	<10	<10	<10	0.92
				41	<10	<10	<10	0.26
2Bp33F	SK028	2.9	<0.7	0	<10	<10	<10	<0.15
				7	<10	<10	<10	<0.15
				14	<10	<10	<10	<0.15
				24	28	<10	<10	2.92
				27	33	<10	<10	3.56
				41	19	<10	11	1.74
2Bp24G	SK012	<0.7	1.9	0	<10	<10	<10	<0.15
				7	<10	<10	<10	<0.15
				14	<10	<10	<10	<0.15
				24	12	<10	<10	14.91
				27	10	<10	<10	13.18
				41	<10	<10	<10	11.05

1 = All monkeys were inoculated with 10<sup>6</sup> PFU of RSV 2B ts virus, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 16 (continued)  
 RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 2B *ts* Mutants<sup>1</sup>

		<i>ts</i> Mutant <u>Virus Growth</u>		<u>Immunogenicity</u>				
<u>Virus</u>	<u>AGM</u>	<u>Peak Virus Titer</u> (log10 PFU/ml)		<u>Day</u>	<u>Neutralization</u> <u>Titers<sup>2</sup></u>			<u>EIA</u> <u>Titers<sup>3</sup></u> (x10 <sup>3</sup> )
		<u>Nasal</u>	<u>Lung</u>		<u>2B</u>	<u>A2</u>	<u>3A</u>	<u>anti-F</u>
2Bp24G	SK030	3.2	<0.7	0	<10	<10	<10	<0.15
				7	<10	<10	<10	<0.15
				14	<10	<10	<10	<0.15
				24	440	10	204	34.13
				27	404	21	190	37.64
				41	256	<10	98	17.74
2Bp20L	SK033	<0.7	<0.7	0	<10	<10	<10	0.24
				7	<10	<10	<10	0.30
				14	<10	<10	<10	1.48
				24	<10	<10	<10	1.64
				27	<10	<10	<10	1.24
				41	<10	<10	<10	0.34
2Bp20L	SK042	<0.7	<0.7	0	<10	<10	<10	<0.15
				7	<10	<10	<10	<0.15
				14	<10	<10	<10	<0.15
				24	<10	<10	<10	1.64
				27	<10	<10	<10	0.20
				41	<10	<10	<10	0.15

1 = All monkeys were inoculated with 10<sup>6</sup> PFU of RSV 2B *ts* virus, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 17  
 RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 2B Challenge of Monkeys 8 Weeks Post-Vaccinated with  
 RSV 2B ts Mutants<sup>1</sup>

		Challenge Virus Growth		Immunogenicity				
		Peak Virus Titer		Day	Neutralization Titers <sup>2</sup>			EIA Titers <sup>3</sup>
Vaccine Virus	AGM	Nasal	Lung		2B	A2	3A	(x10 <sup>3</sup> ) anti-F
2Bp33F	SK034	5.7	5.0	0	<10	<10	<10	0.52
				7	<10	<10	<10	0.91
				14	451	10	472	303.84
				21	6797	33	829	592.61
				28	4353	50	815	135.85
				42	1978	44	264	52.76
2Bp33F	SK028	<0.8	3.8	0	13	<10	<10	2.50
				7	208	65	576	43.64
				14	2868	443	2051	131.70
				21	1883	404	2344	144.39
				28	1127	227	2797	53.22
				42	941	79	729	43.30
2Bp24G	SK012	3.9	3.2	0	<10	<10	<10	21.58
				7	281	111	323	258.89
				14	604	431	731	551.49
				21	698	298	692	668.50
				28	357	325	985	189.81
				42	272	82	895	104.16

- 1 = AGMs were previously vaccinated with RSV 2B ts strains.  
 All monkeys were challenged 8 weeks post-vaccination with  
 10<sup>6</sup> PFU of RSV 2B, IN+IT.
- 2 = 60% plaque reduction neutralization test.
- 3 = Source of coating protein is RSV A2 F protein.

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Table 17 (continued)  
 RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 2B Challenge of Monkeys 8 Weeks Post-Vaccinated with  
 RSV 2B ts Mutants<sup>1</sup>

		Challenge		Immunogenicity				
		<u>Virus Growth</u>						
		<u>Peak Virus</u>						
		<u>Titer</u>						
		(log10 PFU/ml)						
<u>Vaccine</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>	<u>Day</u>	<u>Neutralization</u>			<u>EIA</u>
<u>Virus</u>					<u>Titers<sup>2</sup></u>			<u>Titers<sup>3</sup></u>
								(x10 <sup>3</sup> )
2Bp24G	SK030	<0.8	<0.7	0	91	<10	69	34.55
				7	628	322	1120	174.07
				14	1617	397	1953	203.58
				21	1184	256	968	145.71
				28	851	276	1313	49.28
				42	637	48	329	27.36
2Bp20L	SK033	5.3	4.5	0	<10	<10	<10	1.78
				7	<10	<10	<10	1.88
				14	516	<10	325	289.94
				21	500	22	550	418.91
				28	783	56	525	148.25
				42	518	48	442	91.39
2Bp20L	SK042	5.4	3.3	0	<10	<10	<10	0.21
				7	<10	<10	<10	0.32
				14	36	<10	116	135.80
				21	213	21	284	116.99
				28	256	30	300	30.06
				42	516	40	289	19.30

1 = AGMs were previously vaccinated with RSV 2B ts strains.

All monkeys were challenged 8 weeks post-vaccination with  
 10<sup>6</sup> PFU of RSV 2B, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 17 (continued)

RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 2B Challenge of Monkeys 8 Weeks Post-Vaccinated with  
 RSV 2B *ts* Mutants<sup>1</sup>

		Challenge		Immunogenicity				
		<u>Virus Growth</u>						
		<u>Peak Virus</u>						
		<u>Titer</u>						
		(log10 PFU/ml)						
<u>Vaccine</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>	<u>Day</u>	<u>2B</u>	<u>A2</u>	<u>3A</u>	<u>anti-F</u>
Control	SK046	5.9	4.7	0	<10	<10	<10	0.10
				7	<10	<10	<10	0.13
				14	272	50	594	275.33
				21	488	98	1140	587.93
				28	1377	75	1393	190.49
				42	1659	47	573	183.97
Control	032B	5.5	3.9	0	<10	<10	<10	0.25
				7	<10	<10	<10	0.24
				14	2462	201	3458	626.57
				21	1546	303	1279	482.31
				28	1162	104	1729	164.53
				42	1044	83	689	75.1

1 = AGMs were previously vaccinated with RSV 2B *ts* strains.  
 All monkeys were challenged 8 weeks post-vaccination with  
 10<sup>6</sup> PFU of RSV 2B, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 18  
RSV Growth and Immunogenicity in African Green Monkeys:  
RSV 3A ts Mutants<sup>1</sup>

		<u>ts Mutant</u> <u>Virus Growth</u>		<u>Immunogenicity</u>				
		<u>Peak Virus</u> <u>Titer</u> (log10 PFU/ml)		<u>Day</u>	<u>Neutralization</u> <u>Titers<sup>2</sup></u>			<u>EIA</u> <u>Titers<sup>3</sup></u> (x10 <sup>3</sup> )
<u>Virus</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>		<u>2B</u>	<u>A2</u>	<u>3A</u>	<u>anti-F</u>
3Ap20E	01128	1.7	1.3	0	<10	<10	<10	<0.05
				7	<10	<10	<10	<0.05
				14	<10	<10	<10	3.72
				21	38	<10	39	23.12
				28	21	<10	13	27.42
				40	14	<10	<10	31.11
3Ap20E	0L1161	2.3	2.9	0	<10	<10	<10	<0.05
				7	<10	<10	<10	<0.05
				14	<10	<10	30	5.84
				21	14	12	57	19.51
				28	56	18	126	27.53
				40	44	31	108	38.90
3Ap20F	90B037	3.2	<1.0	0	<10	<10	<10	<0.05
				7	<10	<10	<10	<0.05
				14	<10	<10	11	1.17
				21	12	<10	47	34.32
				28	20	17	86	31.58
				40	49	26	123	35.05

1 = All monkeys were inoculated with 10<sup>6</sup> PFU of RSV 3A ts virus, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 18 (continued)  
 RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 3A *ts* Mutants<sup>1</sup>

		<u><i>ts</i> Mutant Virus Growth</u>		<u>Immunogenicity</u>				
		<u>Peak Virus Titer</u> (log10 PFU/ml)		<u>Day</u>	<u>Neutralization Titers<sup>2</sup></u>			<u>EIA Titers<sup>3</sup></u> (x10 <sup>3</sup> ) <u>anti-F</u>
<u>Virus</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>		<u>2B</u>	<u>A2</u>	<u>3A</u>	
3Ap20F	90B045	3.9	1.0	0	<10	<10	<10	0.35
				7	<10	<10	<10	0.30
				14	<10	<10	19	3.16
				21	11	11	22	12.61
				28	12	13	24	16.82
				40	24	<10	39	14.92
3Ap28F	91B027	2.0	<0.8	0	<10	<10	<10	<0.05
				7	<10	<10	<10	<0.05
				14	<10	<10	<10	0.18
				21	<10	<10	<10	1.29
				28	<10	<10	<10	2.63
				40	<10	11	27	3.83
3Ap28F	91B043 <sup>4</sup>	2.9	<0.9	0	<10	<10	<10	<0.05
				7	<10	<10	<10	<0.05
				14	<10	11	27	3.83

1 = All monkeys were inoculated with 10<sup>6</sup> PFU of RSV 3A *ts* virus, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

4 = Monkey died on day 15. Cause of death unrelated to RSV infection.

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Table 19  
 RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 3A Challenge of Monkeys 8 Weeks Post-Vaccinated with  
 RSV 3A *ts* Mutants<sup>1</sup>

		Challenge		Immunogenicity				
		<u>Virus Growth</u>						
		<u>Peak Virus</u>						
		<u>Titer</u>						
		(log10 PFU/ml)						
<u>Vaccine</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>	<u>Day</u>	<u>2B</u>	<u>A2</u>	<u>3A</u>	<u>anti-F</u>
<u>Virus</u>								(x10 <sup>3</sup> )
3Ap20E	01128	1.4	0.7	0	14	12	<10	35.75
				7	216	281	602	699.10
				14	417	265	784	611.24
				21	289	307	573	247.16
				28	263	289	731	463.57
				42	145	141	426	285.47
3Ap20E	0L1161	2.2	<0.8	0	21	<10	56	25.37
				7	526	412	2735	535.05
				14	516	521	2382	252.93
				21	581	473	1840	275.32
				28	478	437	1651	244.01
				42	250	239	753	141.33
3Ap20F	90B03	<1.1	<0.8	0	84	56	221	41.17
				7	2374	2093	6051	435.25
				14	3701	2916	8652	450.55
				21	2933	2224	6561	481.99
				28	1849	1588	4031	287.28
				42	3086	967	3950	207.98

1 = AGMs were previously vaccinated with RSV 3A *ts* strains. All monkeys were challenged 8 weeks post-vaccination with 10<sup>6</sup> PFU of RSV 3A, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 19 (continued)  
 RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 3A Challenge of Monkeys 8 Weeks Post-Vaccinated with  
 RSV 3A *ts* Mutants<sup>1</sup>

		Challenge Virus Growth		Immunogenicity				
		Peak Virus Titer (log10 PFU/ml)		Day	Neutralization Titers <sup>2</sup>			EIA Titers <sup>3</sup> (x10 <sup>3</sup> )
Vaccine Virus	AGM	Nasal	Lung		2B	A2	3A	anti-F
3Ap20F	90B045	<1.0	<0.8	0	24	12	56	13.44
				7	644	627	1381	182.99
				14	1024	549	2174	223.70
				21	1835	699	2130	273.87
				28	831	318	1499	177.21
				42	534	258	1073	127.80
3Ap28F	91B027	<1.0	0.8	0	<10	<10	<10	5.50
				7	408	229	521	150.97
				14	585	560	2016	234.25
				21	449	311	1161	359.53
				28	316	400	714	184.91
				42	242	217	436	142.67
Control	91K041	5.0	4.7	0	<10	<10	<10	<0.05
				7	<10	<10	<10	0.13
				14	19	<10	205	213.29
				21	106	33	423	602.54
				28	123	99	278	562.05
				42	107	80	277	252.99

1 = AGMs were previously vaccinated with RSV 3A *ts* strains. All monkeys were challenged 8 weeks post-vaccination with 10<sup>6</sup> PFU of RSV 3A, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 19 (continued)

RSV Growth and Immunogenicity in African Green Monkeys:  
 RSV 3A Challenge of Monkeys 8 Weeks Post-Vaccinated with  
 RSV 3A ts Mutants<sup>1</sup>

		Challenge		Immunogenicity				
		<u>Virus Growth</u>						
		<u>Peak Virus</u>						
		<u>Titer</u>						
		(log10 PFU/ml)						
<u>Vaccine</u>	<u>AGM</u>	<u>Nasal</u>	<u>Lung</u>	<u>Day</u>	<u>Neutralization</u>			<u>EIA</u>
<u>Virus</u>					<u>Titers<sup>2</sup></u>			<u>Titers<sup>3</sup></u>
								(x10 <sup>3</sup> )
								<u>anti-F</u>
Control	91K059	5.1	4.6	0	<10	<10	<10	<0.05
				7	<10	<10	<10	0.09
				14	97	34	384	166.59
				21	288	158	1259	268.47
				28	<160	<160	575	286.52
				42	290	178	1448	218.74

1 = AGMs were previously vaccinated with RSV 3A ts strains. All monkeys were challenged 8 weeks post-vaccination with 10<sup>6</sup> PFU of RSV 3A, IN+IT.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 20  
Growth, Immunogenicity, and Efficacy of RSV TS-1 Cotton Rats<sup>1</sup>

<u>Virus</u>	<u>Dose<sup>2</sup></u>	<u>Virus Titer</u>			<u>Immunogenicity</u>				<u>Challenge Virus Titer</u>		
		<u>(log<sub>10</sub> PFU/gm)</u>			<u>Neutralization</u> <sup>2</sup>				<u>(log<sub>10</sub> PFU/gm)</u>		
		<u>#RSV+</u>	<u>Nose</u>	<u>Lung</u>	<u>A2</u>	<u>3A</u>	<u>2B</u>	<u>EIA-F<sup>2</sup></u>	<u>#RSV+</u>	<u>Nose</u>	<u>Lung</u>
A2	5.5	4/4	3.6	4.0	234	367	188	1259	0/4	<1.8	<1.3
TS-1	5.9	4/4	≤2.7	2.3	100	385	181	2071	0/3	<1.9	<1.3
PBS					<10	<10	<10	<50	4/4	4.5	4.8

1 = Cotton rats were inoculated with virus by intranasal route. Four days post-infection, lungs and nasal turbinates were harvested for virus titrations. Six weeks post-infection, blood was taken for neutralization and EIA titrations and rats were challenged intranasally with 10<sup>6</sup> PFU of RSV A2.

Lungs and nasal turbinates were harvested 4 days post-challenge. Virus and antibody titers are reported as geometric mean titers.

2 = 60% plaque reduction neutralization test.

3 = Source of coating protein is RSV A2 F protein.

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Table 21  
Sequence comparison between RSV 2B and 2B33F strains

Gene/ region	Nucl. pos.†	Nucleotide changes			Amino acid changes
	3' end of vRNA	RSV 2B	RSV 2B33F	RSV 2B33F TS(+), 5a revertant	
Genomic Promoter	4 6	C -	G extra A	G extra A	non-coding non-coding
M	4175 4199	T T	C C	C C	non-coding non-coding
SH	4329 4409 4420 4442 4454 4484 4497 4505 4525 4526 4542 4561 4575 4598	T T T T T T T T T T T T T T	C C C C C C C C C C C C C C	C C C C C C C C C C C C C C	Phe-Leu (10) none Ile (36) Ile-Thr (40) none His (47) none Cys (51) none Tyr (61) Stop-Gln (66) none Ser (68) Ile-Thr (75) Ile-Thr (75) Stop-Gln (81) Leu-Pro (87) Trp-Arg (92) none Thr (99)
L	9559 9853* 12186 14587 15071	G A G C A	A G A T G	A A A T G	Arg-Lys (353) Lys-Arg (451)* Asp-Asn (1229) Thr-Ile (2029) non-coding

† For 2B33F and 2B33F TS(+), nucl. pos. numbers are one larger than for 2B for M, SH & L genes

\* At pos. 9853, the Lys-Arg change has reverted back to Lys in the 2B33F TS(+) strain

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Table 22  
Sequence comparison between RSV 2B and 2B20L strains

Gene/ region	Nucl. pos.†	Nucleotide changes			Amino acid changes
		RSV 2B	RSV 2B20L	RSV 2B20L TS(+), R1 revertant	
Genomic Promoter	4 6	C -	G extra A	G extra A	non-coding* non-coding*
L	8963 13347 14587 14649 14650	C A C A A	T A T G A	T G T G T	none Thr (154) Asn-Asp (1616) Thr-Ile(2029)* Asn-Asp (2050) Asn-Asp-Val (2050)**

- † For 2B20L and 2B20L TS(+), nucl. pos. numbers are one larger than for 2B for L gene
- \* Mutation is common in 2B33F and 2B20L strains
- \*\* At pos. 14650, the mutation suppresses the ts phenotype in 2B20L TS(+) revertant

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Table 23  
RSV 2B, *ts* and Revertant Strains

Sample	Source	In Vitro Phenotype <i>ts</i>		In Vivo Growth* Cotton Rat				AGM
		39/32°C EOP plaque morph	20/32°C Yield	Nasal turbينات	Lungs	Nasal Wash	Bronchial Lavage	
RSV 2B	Wild-type Parent Strain	0.7 (WT)	0.0001	5.5 <sup>a</sup> 3.9 <sup>b</sup> (4/4)	5.8 <sup>a</sup> 5.2 <sup>b</sup> (4/4)	5.8 <sup>a</sup> (4/4)	4.7 <sup>a</sup> (4/4)	
RSV 2B33F	ca, <i>ts</i> mutant isolated from 2B cold-passaged x 33	0.00007 (sp/int/wt)	0.04	≤1.6 <sup>a</sup> <1.9 <sup>b</sup> (1/4)	<1.5 <sup>a</sup> <1.2 <sup>b</sup> (0/4)	3.0 <sup>a</sup> (4/4)	<0.9 <sup>a</sup> (0/4)	
RSV 2B33F - 5a TS(+)	2B33F spinner passage, plaque picked at 39°C	0.5 (WT)	0.03	≤1.7 <sup>a</sup> (1/4)	3.5 <sup>a</sup> (4/4)	4.2 <sup>a</sup> (4/4)	4.0 <sup>a</sup> (4/4)	
RSV 2B33F - 4a TS(+)	2B33F spinner passage, plaque picked at 39°C	0.7 (WT)	0.01	≤1.7 <sup>a</sup> (3/4)	3.8 <sup>a</sup> (4/4)	ND	ND	
RSV 2B33F - 3b TS(+)	2B33F spinner passage, plaque picked at 39°C	0.5 (WT)	0.04	≤2.5 <sup>a</sup> (3/4)	2.9 <sup>a</sup> (4/4)	ND	ND	
AGM pp2	2B33F-infected AGM #A2,d7 nasal wash plaque picked at 32°C	0.3 (sp,int)	0.00002	≤2.0 <sup>b</sup> (1/4)	1.6 <sup>b</sup> (4/4)	ND	ND	

Table 23 (continued)  
RSV 2B, ts and Revertant Strains

Sample	Source	In Vitro Phenotype <sup>ca</sup>		In Vivo Growth* Cotton Rat				AGM
		39/32°C EOP plaque morph	20/32°C Yield	Nasal turbينات	Lungs	Nasal Wash	Bronchial Lavage	
AGM pp4	2B33F-infected AGM #A2, d7 nasal wash plaque picked at 32°C	0.1 (sp,int)	0.008	<1.6 <sup>b</sup> (0/4)	1.2 <sup>b</sup> (4/4)	ND	ND	ND
AGM pp6	2B33F-infected AGM #A4, d12 nasal wash plaque picked at 32°C	0.000004 (wt)	≤0.00005	≤1.5 <sup>b</sup> (1/4)	<1.1 <sup>b</sup> (0/4)	ND	ND	ND
AGM pp7	2B33F-infected AGM #A4, d12 nasal wash plaque picked at 32°C	0.000004 (sp/int/wt)	0.007	≤1.4 <sup>b</sup> (1/4)	<1.0 <sup>b</sup> (0/4)	ND	ND	ND
Chimp pp1A	2B33F-infected Chimp #1552, d4 tracheal lavage plaque picked at 32°C	0.5 (WT)	ND	ND	ND	ND	ND	ND
Chimp pp3A	2B33F-infected Chimp #1560, d6 tracheal lavage plaque picked at 32°C	0.7 (WT)	ND	2.4 <sup>c</sup> (4/4)	≤3.0 <sup>c</sup> (3/4)	ND	ND	ND
Chimp pp5A	2B33F-infected Chimp #1563, d10 nasal swab plaque picked at 32°C	0.7 (WT)	ND	≤2.3 <sup>c</sup> (3/4)	3.0 <sup>c</sup> (4/4)	ND	ND	ND

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Table 23 (continued)  
RSV 2B, ts and Revertant Strains

Sample	Source	In Vitro Phenotype ts		In Vivo Growth* Cotton Rat			
		39/32°C EOP plaque morph	20/32°C Yield	Nasal turbinate	Lungs	Nasal Wash	Bronchial Lavage
RSV 2B20L	ca, ts mutant isolated from 2B cold-passaged x 20	0.0002 (int/wt)	0.02	<1.9 <sup>d</sup> (0/4)	<1.3 <sup>d</sup> (0/4)	<0.7 <sup>f</sup> (0/2)	<0.7 <sup>f</sup> (0/2)
RSV 2B20L R1 TS(+)	2B20L spinner passage, plaque picked at 39°C	0.6 (WT)	ND	2.3 <sup>c</sup> (4/4)	3.5 <sup>c</sup> (4/4)	ND	ND
RSV 2B20L R2 TS(+)	2B20L spinner passage, plaque picked at 39°C	0.6 (WT)	ND	≤2.5 <sup>c</sup> (3/4)	2.7 <sup>c</sup> (4/4)	ND	ND
RSV 2B20L R9 TS(+)	2B20L spinner passage, plaque picked at 39°C	0.8 (WT)	ND	≤2.2 <sup>c</sup> (3/4)	4.0 <sup>c</sup> (4/4)	ND	ND
RSV 2B20L R10 TS(+)	2B20L spinner passage, plaque picked at 39°C	0.7 (WT)	ND	2.6 <sup>c</sup> (4/4)	3.2 <sup>c</sup> (4/4)	ND	ND

\* In Vivo growth measured in log<sub>10</sub> mean virus titer (# infected/# total)  
 ND = not done WT = wild-type plaque size sp = small plaque size int = intermediate  
 plaque size  
 a Dose = 10<sup>5.7</sup> PFU IN ° Dose = 10<sup>6.3</sup> PFU IN  
 d Dose = 10<sup>5.9</sup> PFU IN ° Dose = 10<sup>6.0</sup> PFU IN+IT

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Table 24  
2B33F Revertants

	<i>ts</i> (+) <i>In vitro</i>			AGM				Chimp		
	5a	4a	3b	pp2	pp4	pp6	pp7	1A	3A	5A
base no.†										
<u>M</u>										
4176,4200	S	S	S	S	S	S	S	S	S	S
<u>SH</u>										
14 bases*	S	S	S	S	S	S	S	S	S	S
<u>L</u>										
9560	S	S	S	S	S	S	S	S	S	S
9854	2B	2B	2B	S	S	S	S	2B	2B	2B
12187	S	S	S	S	S	S	S	S	S	S
14588	S	S	S	S	S	S	S	S	S	S
15072	S	S	S	S	S	S	S	S	S	S
Phenotype										
<i>ts</i>	2B	2B	2B	r	r	S	S	2B	2B	2B
<i>ca</i>	S	S	S	2B	S	2B	S	ND	ND	ND
Attenuated	r	r	r	(r)	(r)	S	S	ND	r	r

† These 2B33F revertant base nos. are one larger than for 2B for M, SH and L genes

\* bases 4330,4410,4421,4443,4455,4485,4498,4506,4526,4527,4543,4562,4576,4599

S = same base as 2B33F

2B = reversion to 2B base or complete reversion in phenotype

r = moderate reversion in phenotype

(r) = slight reversion in phenotype

ND = not done

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Table 25  
2B20L Revertants

base no.†	TS(+) In vitro Isolates									
	R1	R2	R3A	R4A	R5A	R6A	R7A	R8A	R9A	R10A
<u>L</u>										
8964	S	S	S	S	S	S	S	S	S	S
13348	C*	S	ND	S	S	ND	S	S	S	S
14588	S	S	S	S	S	S	S	S	S	S
14650	S	S	2B	S	2B	2B	S	S	2B	2B
14651	A*	A*	S	A*	S	S	A*	A*	S	S
Phenotype										
ts	2B	2B	ND	ND	ND	ND	ND	ND	2B	2B
Attenuated	r	r	ND	ND	ND	ND	ND	ND	r	r

† These 2B20L revertant base nos. are one larger than for 2B for L genes

S = same base as 2B20L

2B = reversion to 2B base

r = moderate reversion in phenotype

\* = base change, different from 2B or 2B20L

ND = not done

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Table 26  
RSV 2B, *ts* and Revertant Strains: Phenotype Summary

Virus Isolate	Source	In Vitro Phenotype		In Vivo Attenuation	
		<i>ts</i>	<i>ca</i>	Cotton Rat	AGM
RSV 2B	Wild-type Parent Strain	-	-	-	-
RSV 2B33F	<i>ca</i> , <i>ts</i> mutant isolated from 2B, cold-passaged x 33	++++	++	++++	+++
RSV 2B33F - 5a TS(+)	2B33F spinner passage plaque picked at 39°C	-	++	++	+
RSV 2B33F - 4a TS(+)	2B33F spinner passage plaque picked at 39°C	-	++	++	ND
RSV 2B33F - 3b TS(+)	2B33F spinner passage plaque picked at 39°C	-	++	++	ND
AGM pp2	2B33F-infected AGM A2, d7 nasal wash plaque picked at 32°C	+	-	+++	ND
AGM pp4	2B33F-infected AGM A2, d7 nasal wash plaque picked at 32°C	+	++	+++	ND
AGM pp6	2B33F-infected AGM A4, d12 nasal wash plaque picked at 32°C	++++	-	++++	ND
AGM pp7	2B33F-infected AGM A4, d12 nasal wash plaque picked at 32°C	++++	++	++++	ND
Chimp pp1A	2B33F-infected chimp #1552, d4 tracheal lavage, plaque picked at 32°C	-	ND	ND	ND
Chimp pp3A	2B33F-infected chimp #1560, d6 tracheal lavage, plaque picked at 32°C	-	ND	++	ND
Chimp pp5A	2B33F-infected chimp #1563, d10 tracheal lavage, plaque picked at 32°C	-	ND	++	ND

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Table 26 (continued)  
RSV 2B, ts and Revertant Strains: Phenotype Summary

Virus Isolate	Source	In Vitro Phenotype		In Vivo Attenuation	
		ts	ca	Cotton Rat	AGM
RSV 2B20L	ca, ts mutant isolated from 2B, cold-passaged x 20	++++	++	++++	++++
RSV 2B20L R1 TS(+)	2B20L spinner passage plaque picked at 39°C	-	ND	++	ND
RSV 2B20L R2 TS(+)	2B20L spinner passage plaque picked at 39°C	-	ND	++	ND
RSV 2B20L R9 TS(+)	2B20L spinner passage plaque picked at 39°C	-	ND	++	ND
RSV 2B20L R10 TS(+)	2B20L spinner passage plaque picked at 39°C	-	ND	++	ND

ND = not done

- = wild-type phenotype, i.e., not temperature sensitive, not cold-adapted, not attenuated

+ to ++++ = increasing levels of temperature sensitivity, cold-adaptation or attenuation

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